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(54) **IMMUNOGENIC COMPOSITIONS FOR**
STREPTOCOCCUS AGALACTIAE

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(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

This application relates to Group B *Streptococcus* ("GBS")
vaccines comprising combinations of GBS polypeptide anti-
gens where the polypeptides contribute to the immunological
response in a recipient. Preferably, the compositions of the
invention comprise a combination of two or more GBS anti-
gens, wherein said combination includes GBS 80 or a frag-
ment thereof. In one embodiment, the combination may con-
sist of two to thirteen GBS antigens selected from an antigen
group consisting of GBS 80, GBS 91, GBS 104, GBS 184,
GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361,
GBS 404, GBS 690, and GBS 691.

10 Claims, No Drawings

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IMMUNOGENIC COMPOSITIONS FOR *STREPTOCOCCUS AGALACTIAE*

This application is a national stage application of co-pending PCT application PCT/US2004/030032 filed Sep. 15, 2004, which was published in English under PCT Article 21(2) on Mar. 31, 2004 and which claims priority to Ser. No. 60/548,789, filed Feb. 26, 2004 and is a continuation-in-part of PCT/US2003/029167, filed on Sep. 15, 2003. Each of these applications is incorporated herein by reference in its entirety.

This application incorporates by reference the contents of a 319 kb text file created on Jan. 15, 2010 and named "SN10568422_sequencelisting.txt," which is the sequence listing for this application.

FIELD OF THE INVENTION

The invention relates to an immunogenic antigen derived from *Streptococcus agalactiae* ("GBS") and its use in combinations with other GBS antigens to provide for broader coverage among different GBS strains. In particular, the invention relates to a composition comprising a combination of two or more GBS antigens, wherein the combination includes GBS 80 or a fragment thereof. The combination may include GBS 80 and at least one other GBS antigen. For example, the combination may include GBS 80 and up to thirteen GBS antigens. In a preferred embodiment, the combination may include GBS 80 and up to ten GBS antigens. In a more preferred embodiment, the combination may include GBS 80 and up to five GBS antigens. In one embodiment, the combination may consist of two to thirteen GBS antigens selected from an antigen group consisting of GBS 80, GBS 91, GBS 104, GBS 184, GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361, GBS 404, GBS 690, and GBS 691. Preferably, the combination includes GBS 80 in combination with one or more of GBS 104 and GBS 322.

BACKGROUND OF INVENTION

GBS has emerged in the last 20 years as the major cause of neonatal sepsis and meningitis that affect 0.5-3 per 1000 live births, and an important cause of morbidity among the older age group affecting 5-8 per 100,000 of the population. Current disease management strategies rely on intrapartum antibiotics and neonatal monitoring which have reduced neonatal case mortality from >50% in the 1970's to less than 10% in the 1990's. Nevertheless, there is still considerable morbidity and mortality and the management is expensive. 15-35% of pregnant women are asymptomatic carriers and at high risk of transmitting the disease to their babies. Risk of neonatal infection is associated with low serotype specific maternal antibodies and high titers are believed to be protective. In addition, invasive GBS disease is increasingly recognized in elderly adults with underlying disease such as diabetes and cancer.

The "B" in "GBS" refers to the Lancefield classification, which is based on the antigenicity of a carbohydrate which is soluble in dilute acid and called the C carbohydrate. Lancefield identified 13 types of C carbohydrate, designated A to O, that could be serologically differentiated. The organisms that most commonly infect humans are found in groups A, B, D, and G. Within group B, strains can be divided into at least 9 serotypes (Ia, Ib, Ia/c, II, m, IV, V, VI, VII and VIII) based on the structure of their polysaccharide capsule. In the past, serotypes Ia, Ib, II, and III were equally prevalent in normal vaginal carriage and early onset sepsis in newborns. Type V

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GBS has emerged as an important cause of GBS infection in the USA, however, and strains of types VI and VIII have become prevalent among Japanese women.

The genome sequence of a serotype V strain 2603 V/R has been published (Ref. 1) and various polypeptides for use as vaccine antigens have been identified (Ref. 2). The vaccines currently specificity and poor immunogenicity, and so there is a need for effective vaccines against *S. agalactiae* infection.

It is an object of the invention to provide further and improved compositions for providing immunity against GBS disease and/or infection. The compositions are based on a combination of two or more (e.g., three or more) GBS antigens.

SUMMARY OF THE INVENTION

Applicants have discovered that an immunogenic GBS antigen, GBS 80, is particularly suitable for immunization purposes, especially when used in combination with other GBS antigens. The combination may include GBS 80 and at least one other GBS antigen or up to thirteen other GBS antigens. In a preferred embodiment, the combination may include GBS 80 and up to 10 GBS antigens. In a more preferred embodiment, the combination includes GBS 80 and up to five GBS antigens. In particular, the invention relates to a composition comprising a combination of two or more GBS antigens, wherein the combination includes GBS 80 or a fragment thereof. In one embodiment, the combination may consist of two to thirteen GBS antigens selected from the group consisting of GBS 80, GBS 91, GBS 104, GBS 184, GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361, GBS 404, GBS 690, and GBS 691. Preferably, the combination consists of GBS 80, GBS 104 and GBS 322.

Instead of the full length antigen, the combination may comprise an immunogenic fragment of the selected GBS antigen and/or a polypeptide sequence having sequence identity to the selected antigen.

Preferably, the combination of GBS antigens consists of three, four, five, six, seven, eight, nine, or ten GBS antigens. Still more preferably, the combination of GBS antigens consists of three, four, or five GBS antigens.

DETAILED DESCRIPTION OF THE INVENTION

The practice of the present invention will employ, unless otherwise indicated, conventional methods of chemistry, biochemistry, molecular biology, immunology and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., *Remington's Pharmaceutical Sciences*, Mack Publishing Company, Easton, Pa., 19th Edition (1995); *Methods In Enzymology* (S. Colowick and N. Kaplan, eds., Academic Press, Inc.); and *Handbook of Experimental Immunology*, Vols. I-IV (D. M. Weir and C. C. Blackwell, eds., 1986, Blackwell Scientific Publications); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Handbook of Surface and Colloidal Chemistry* (Birdi, K. S. ed., CRC Press, 1997); *Short Protocols in Molecular Biology*, 4th ed. (Ausubel et al. eds., 1999, John Wiley & Sons); *Molecular Biology Techniques: An Intensive Laboratory Course*, (Ream et al., eds., 1998, Academic Press); *PCR (Introduction to Biotechniques Series)*, 2nd ed. (Newton & Graham eds., 1997, Springer Verlag); Peters and Dalrymple, *Fields Virology* (2d ed), Fields et al. (eds.), B. N. Raven Press, New York, N.Y.

All publications, patents and patent applications cited herein, are hereby incorporated by reference in their entireties.

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GBS Antigens

As discussed above, the invention provides an immunogenic composition comprising a combination of two or more GBS antigens, wherein said combination includes GBS 80 or a fragment thereof.

The combinations of GBS antigens may include polypeptide fragments of the identified GBS antigens. The length of the fragment may vary depending on the amino acid sequence of the specific GBS antigen, but the fragment is preferably at least 7 consecutive amino acids, (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more). Preferably the fragment comprises one or more epitopes from the sequence. Other preferred fragments include (1) the N-terminal signal peptides of each identified GBS antigen, (2) the identified GBS antigens without their N-terminal signal peptides, and (3) each identified GBS antigen wherein up to 10 amino acid residues (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) are deleted from the N-terminus and/or the C-terminus e.g. the N-terminal amino acid residue may be deleted. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

The combinations of GBS antigens may include polypeptide sequences having sequence identity to the identified GBS antigens. The degree of sequence identity may vary depending on the amino acid sequence (a) in question, but is preferably greater than 50% (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more). Polypeptides having sequence identity include homologs, orthologs, allelic variants and functional mutants of the identified GBS antigens. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman homology search algorithm as implemented in the MPSRCH program (Oxford Molecular), using an affinity gap search with parameters gap open penalty=12 and gap extension penalty=1.

The polypeptides can, of course, be prepared by various means (e.g. recombinant expression, purification from CBS, chemical synthesis etc.) and in various forms (e.g. native, fusions, glycosylated, non-glycosylated etc.). They are preferably prepared in substantially pure form (i.e. substantially free from other streptococcal or host cell proteins) or substantially isolated form.

GBS 80

As discussed above, the invention relates to the use of GBS 80 in synergistic combination with other GBS antigens. GBS 80 refers to a putative cell wall surface anchor family protein. Nucleotide and amino acid sequence of GBS 80 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8779 and SEQ ID 8780. These sequences are also set forth below as SEQ ID NOS 1 and 2:

SEQ ID NO. 1

ATGAAATTATCGAAGAGGTTATTGTTTTCGGCTGCTGTTTAAACATGGT
GGCGGGGTCAACTGTTGAACAGTAGCTCAGTTTGCAGCTGGAATGAGTA
TTGTAAGAGCTGCAGAAGTGTCACAAGAACGCCAGCGAAACAACAGTA
AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTTCTAA
TGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAAC
TTGGTGACAAATGTAAAGGTTTGAAGGTGTACAGTTTAAACGTTATATAA

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-continued

GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAACAGTTGA
AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTAC
CTCAAAAACTAATGCTCAAGGTTTGGTCGTCGATCTGAGTTCAAAA
AGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCTTCAAA
CATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCTA
ACTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTTACCTTAAAAAC
GTTGTAAGTATGAACCAAAAAACAGATAAAGATGTTAAAAAATTAGGTCA
GGACGATGCAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAAT
CTACAATCCCTGCCAATTTAGTGACTATGAAAAATTTGAAATTACTGAT
AAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAATAATCAAGATTGG
TTGAAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
TTGATAACCAAAATACATTAAAAATTACGTTTAAACAGAGAAATTTAAA
GAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAAAAATCAAGATGC
TCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATTC
CAGTTGCATCAACTATTAATGAAAAAGCAGTTTATAGGAAAGCAATTGAA
AATACTTTTGAACCTTCAATATGACCATACTCTGATAAAGCTGACAATCC
AAAACCATCTAATCCTCCAAGAAAAACAGAGTTTACTACTGGTGGGAAAC
GATTTTGTAAGAAAGACTCAACAGAAACACAAACACTAGGTGGTGTCTGAG
TTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
TATTAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
GGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTTGAGATTAAA
GGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTTA
CAAATTAAGAAACAAAGACAGCAGAGGTTATGTAATCCCTGATAAAG
AAATCGAGTTTACAGTATCACAAACATCTTATAATACAAACCAACTGAC
ATCACGGTTGATAGTGTGATGCAACACCTGATACAAATTAATAAACACAA
ACGTCCTTCAATCCCTAATACTGGTGGTATTGGTACGGCTATCTTTGTCTG
CTATCGGTGCTGCGGTGATGGCTTTTGTCTGTTAAGGGGATGAAGCGTCTG

ACAAAAGATAAC

SEQ ID NO: 2

MKLSKKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSRPAKTTV
NIYKLQADSYKSEITSNGGIENKDGEVINSYAKLGDNVKGLQGVQPKRYK
VKTDISVDELKKLTTVEADAQVGTILEBGVSLPQKTNAGLVVDALDSK
SNVRYLYVEDLKNPSNITKAYAVPFVLELVPANSTGTGFLSEINIYPKN
VVTDEPKTDKDVKKLQDDAGYTI GEEFKWFLKSTIPANLGDYEFKEITD
KFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAI E
NTFELQYDHTPDKADNPKPSNPPRKEVHTGGKRFFVKDSTETQTLGGAE
FDLLASDGTAVKWTDALIKANTKNYIAGEAVTGQPIKLKSHDTGTFEIK
GLAYAVDANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTD
ITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAMAFVKGMKRR
TKDN

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As described above, the combinations of the invention may include a fragment of a GBS antigen. In some instances, removal of one or more domains, such as a leader or signal sequence region, a transmembrane region, a cytoplasmic region or a cell wall anchoring motif, may facilitate cloning of the gene encoding the antigen and/or recombinant expression of the GBS protein. In addition, fragments comprising immunogenic epitopes of the cited GBS antigens may be used in the compositions of the invention.

GBS 80 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 2 above. In one embodiment, one or more amino acids from the leader or signal sequence region of GBS 80 are removed. An example of such a GBS 80 fragment is set forth below as SEQ ID NO: 3:

SEQ ID NO: 3

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDN
VKGLQGVQFKRYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKT
NAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLELPGVANSTG
TGFLSEINIYPKNVVTDEPKTKDKVKKLGQDDAGYTIGEEFKWFLKSTIP
ANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQ
NTLKITFKPEKFEIAELLKGMTLVKNQDALDKATANTDDAAFLIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVK
KDSTETQTLGGAEFDLLASDGTAVKWDALIKANTKNYIAGEAVTGQPI
KLKSHDTGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVIPDKEIEF
TVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPTGGIGTAIFVAIGA
AVMAFAVKGMRRTKDN

GBS 80 contains a C-terminal transmembrane region which is indicated by the underlined sequence near the end of SEQ ID NO: 2 above. In one embodiment, one or more amino acids from the transmembrane region and/or a cytoplasmic region are removed. An example of such a GBS 80 fragment is set forth below as SEQ ID NO: 4:

SEQ ID NO: 4

MKLSKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTV
NIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYK
VKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSK
SNVRYLYVEDLKNSPSNITKAYAVPFVLELPGVANSTGTGFLSEINIYPKN
VVTDEPKTKDKVKKLGQDDAGYTIGEEFKWFLKSTIPANLGDYEKFEITD
KFADGLTYKSVGKIKIGSKYLNDRDEHYTIDEPTVDNQNTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLIPVASTINEKAVLGKAI
NTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLGGAE
FDLLASDGTAVKETDALIKANTKNYIAGEAVTGQPIKLKSHDTGTFEIK
GLAYAVDANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTD
ITVDSADATPDTIKNNKRPSIPTG

GBS 80 contains an amino acid motif indicative of a cell wall anchor: SEQ ID NO: 5 IPNTG (shown in *italics* in SEQ ID NO: 2 above). In some recombinant host cell systems, it may be preferable to remove this motif to facilitate secretion of a recombinant GBS 80 protein from the host cell. Accord-

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ingly, in one preferred fragment of GBS 80 for use in the invention, the transmembrane and/or cytoplasmic regions and the cell wall anchor motif are removed from GBS 80. An example of such a GBS 80 fragment is set forth below as SEQ ID NO: 6.

SEQ ID NO: 6

MKLSKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTV
NIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYK
VKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSK
SNVRYLYVEDLKNSPSNITKAYAVPFVLELPGVANSTGTGFLSEINIYPKN
VVTDEPKTKDKVKKLGQDDAGYTIGEEFKWFLKSTIPANLGDYEKFEITD
KFADGLTYKSVGKIKIGSKYLNDRDEHYTIDEPTVDNQNTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLIPVASTINEKAVLGKAI
NTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLGGAE
FDLLASDGTAVKETDALIKANTKNYIAGEAVTGQPIKLKSHDTGTFEIK
GLAYAVDANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTD
ITVDSADATPDTIKNNKRPS

Alternatively, in some recombinant host cell systems, it may be preferable to use the cell wall anchor motif to anchor the recombinantly expressed protein to the cell wall. The extracellular domain of the expressed protein may be cleaved during purification or the recombinant protein may be left attached to either inactivated host cells or cell membranes in the final composition.

In one embodiment, the leader or signal sequence region, the transmembrane and cytoplasmic regions and the cell wall anchor motif are removed from the GBS 80 sequence. An example of such a GBS 80 fragment is set forth below as SEQ ID NO: 7.

SEQ ID NO: 7

AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDN
VKGLQGVQFKRYKVKTDISVDELKKLTVEAADAKVGTILEEGVSLPQKT
NAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLELPGVANSTG
TGFLSEINIYPKNVVTDEPKTKDKVKKLGQDDAGYTIGEEFKWFLKSTIP
ANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQ
NTLKITFKPEKFEIAELLKGMTLVKNQDALDKATANTDDAAFLIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVK
KDSTETQTLGGAEFDLLASDGTAVKWDALIKANTKNYIAGEAVTGQPI
KLKSHDTGTFEIKGLAYAVDANAEGTAVTYKLKETKAPEGYVIPDKEIEF
TVSQTSYNTKPTDITVDSADATPDTIKNNKRPS

Applicants have identified a particularly immunogenic fragment of the GBS 80 protein. This immunogenic fragment is located towards the N-terminus of the protein and is underlined in the GBS 80 SEQ ID NO: 2 sequence below. The underlined fragment is set forth below as SEQ ID NO: 8.

SEQ ID NO: 8

MKLSKLLFSAAVLTMVAGSTVEPVAQFATGMSIVRAAEVSQERPAKTTV
NIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGLQGVQFKRYK

7

-continued

VKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSK
 SNVRYLVEEDLKNSPSNITKAYAVPFVLELNVANSTGTGLSEINIYPKN
 VVTDEPKTDKDVKKLGQDDAGYTIGEEFKWFLKSTIPANLGDYEKFEITD
 KFADGLTYKSVGKIKIGSKYLNDRDEHYTIDEPTVDNQNTLKITFKPEKFK
 EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAE
 NTFELQYDHTPDKADNPKNPPRKPEVHTGGKRFVKKDSSTETQTLGGAE
 FDLASDGTAVKETDALIKANTNKNYIAGEAVTGQPIKLKSHDTGTFEIK
 GLAYAVDANAEGTAVTYKLKETKAPEGYVIPDKEIETVSQTSYNTKPTD
 ITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAVMAGAVKMKRR
 TKDN

SEQ ID NO: 8

AEVSQERPAKTTVNIYKLDADSYKSEITSGGIENKDGVEISNYAKLGDN
 VKGLQGVQPKRYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKT
 NAQGLVVDALDSKSNVRYLVEEDLKNSPSNITKAYAVPFVLELNVANSTG
 TGLSEINIYPKNVVTDEPKTDKDVKKLGQDDAGYTIGEEFKWFLKSTIP
 ANLGDYEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQ
 NTLKITFKPEKFEIAELLKG

The immunogenicity of the protein encoded by SEQ ID NO: 7 was compared against PBS, GBS whole cell, GBS 80 (full length) and another fragment of GBS 80, located closer to the C-terminus of the peptide (SEQ ID NO: 9, below).

SEQ ID NO: 9

MTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAEINTFELQYD
 HTPDKADNPKNPPRKPEVHTGGKRFVKKDSSTETQTLGGAEFDLLASDG
 TAVKWDALIKANTNKNYIAGEAVTGQPIKLKSHDTGTFEIKGLAYAVDA
 NAEGTAVTYKLKETKAPEGYVIPDKEIETVSQTSYNTKPTDITVDSADA
 TPTDTIKNNKRPS

Both an Active Maternal Immunization Assay and a Passive Maternal Immunization Assay were conducted on this collection of proteins.

As used herein, an Active Maternal Immunization assay refers to an in vivo protection assay where female mice are immunized with the test antigen composition. The female mice are then bred and their pups are challenged with a lethal dose of GBS. Serum titers of the female mice during the immunization schedule are measured as well as the survival time of the pups after challenge.

Specifically, the Active Maternal Immunization assays referred to herein used groups of four CD-1 female mice (Charles River Laboratories, Calco Italy). These mice were immunized intraperitoneally with the selected proteins in Freund's adjuvant at days 1, 21 and 35, prior to breeding. 6-8 weeks old mice received 20 µg protein/dose when immunized with a single antigen, 30-45 µg protein/dose (15 µg each antigen) when immunized with combination of antigens. The immune response of the dams was monitored by using serum samples taken on day 0 and 49. The female mice were bred 2-7 days after the last immunization (at approximately t=36-37), and typically had a gestation period of 21 days. Within 48 hours of birth, the pups were challenged via I.P. with GBS in a dose approximately equal to an amount which would be

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sufficient to kill 70-90% of unimmunized pups (as determined by empirical data gathered from PBS control groups). The GBS challenge dose is preferably administered in 50 µl of THB medium. Preferably, the pup challenge takes place at 56 to 61 days after the first immunization. The challenge inocula were prepared starting from frozen cultures diluted to the appropriate concentration with THB prior to use. Survival of pups was monitored for 5 days after challenge.

As used herein, the Passive Maternal Immunization Assay refers to an in vivo protection assay where pregnant mice are passively immunized by injecting rabbit immune sera (or control sera) approximately 2 days before delivery. The pups are then challenged with a lethal dose of GBS.

Specifically, the Passive Maternal Immunization Assay referred to herein used groups of pregnant CD1 mice which were passively immunized by injecting 1 ml of rabbit immune sera or control sera via I.P., 2 days before delivery. Newborn mice (24-48 hrs after birth) are challenged via I.P. with a 70-90% lethal dose of GBS serotype III COH1. The challenge dose, obtained by diluting a frozen mid log phase culture, was administered in 50 µl of THB medium.

For both assays, the number of pups surviving GBS infection was assessed every 12 hrs for 4 days. Statistical significance was estimated by Fisher's exact test.

The results of each assay for immunization with SEQ ID NO: 7, SEQ ID NO: 8, PBS and GBS whole cell are set forth in Tables 1 and 2 below.

TABLE 1

Active Maternal Immunization

Antigen	Alive/total	% Survival	Fisher's exact test
PBS (neg control)	13/80	16%	
GBS (whole cell)	54/65	83%	P < 0.00000001
GBS80 (intact)	62/70	88%	P < 0.00000001
GBS80 (fragment) SEQ ID 7	35/64	55%	P = 0.0000013
GBS80 (fragment) SEQ ID 8	13/67	19%	P = 0.66

TABLE 2

Passive Maternal Immunization

Antigen	Alive/total	% Survival	Fisher's exact test
PBS (neg control)	12/42	28%	
GBS (whole cell)	48/52	92%	P < 0.00000001
GBS80 (intact)	48/55	87%	P < 0.00000001
GBS80 (fragment) SEQ ID 7	45/57	79%	P = 0.0000006
GBS80 (fragment) SEQ ID 8	13/54	24%	P = 1

As shown in Tables 1 and 2, immunization with the SEQ ID NO: 7 GBS 80 fragment provided a substantially improved survival rate for the challenged pups than the comparison SEQ ID NO: 8 GBS 80 fragment. These results indicate that the SEQ ID NO: 7 GBS 80 fragment may comprise an important immunogenic epitope of GBS 80.

Combinations Including GBS 80

The invention includes combinations of two or more GBS antigens wherein the combination includes GBS 80 or a fragment thereof. Applicants have discovered that GBS 80 is particularly suitable for immunization in combination with other GBS antigens and that these antigen combinations provide for a broader coverage among different GBS strains.

Preferably, the combination of GBS antigens consists of three, four, five, six, seven, eight, nine, or ten GBS antigens.

Still more preferably, the combination of GBS antigens consists of three, four, or five GBS antigens.

Preferably, the combinations of the invention provide for improved immunogenicity over the immunogenicity of the antigens when administered alone. Improved immunogenicity may be measured, for example, by the Active Maternal Immunization Assay. As discussed above, this assay may be used to measure serum titers of the female mice during the immunization schedule as well as the survival time of the pups after challenge. Preferably, immunization with the immunogenic compositions of the invention yield an increase of at least 2 percentage points (preferably at least 3, 4 or 5 percentage points) in the percent survival of the challenged pups as compared to the percent survival from maternal immunization with a single antigen of the composition when administered alone. Preferably, the increase is at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 percentage points. Preferably, the GBS combinations of the invention comprising GBS 80 demonstrate an increase in the percent survival as compared to the percent survival from immunization with a non-GBS 80 antigen alone.

According to one embodiment of the invention, combinations of antigens or fusion proteins containing a portion or portions of the antigens will include GBS 80 or a portion thereof in combination with from one to 10 antigens, preferably one to 10 or less antigens. Such other antigens include by way of example and not limitation, GBS 67, GBS 91, GBS 104, GBS 184, GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361, GBS 404, GBS 690, and GBS 691. Still other antigens are identified in U.S. Ser. No. 10/415,182, filed Apr. 28, 2003, hereby incorporated in its entirety.

Combinations, for example, can include GBS 80, GBS 104, GBS 322, and GBS 276; GBS 80, GBS 338, GBS 330; GBS 80, GBS 330, GBS 104; GBS 80, GBS 104, GBS 404; GBS 80, GBS 338, GBS 104; GBS 80, GBS 338, GBS 404; GBS 338, GBS 330, GBS 104; GBS 338, GBS 104, GBS 404; GBS 80, GBS 330, GBS 404; GBS 80, GBS 322, GBS 104; GBS 80, GBS 322, GBS 276; GBS 80, GBS 322, GBS 91; GBS 80, GBS 104, GBS 276; GBS 80, GBS 104, GBS 91; GBS 80, GBS 276, GBS 91; GBS 80, GBS 322, GBS 104; GBS 80, GBS 322, GBS 276; GBS 80, GBS 322, GBS 91; GBS 80, GBS 104, GBS 276; GBS 80, GBS 104, GBS 91; GBS 80, GBS 276, GBS 91; GBS 80, GBS 690, GBS 691; GBS 80, GBS 690, GBS 338; GBS 80, GBS 690, GBS 305; GBS 80, GBS 691, GBS 305; GBS 80, GBS 338, GBS 305; GBS 80, GBS 338, GBS 361; GBS 80, GBS 305, GBS 361; GBS 80, GBS 184, GBS 691; GBS 80, GBS 691, GBS 338; GBS 80, GBS 104, GBS 276, GBS 322; GBS 80, GBS 104, GBS 67, and GBS 322. Examples of combinations of the invention which demonstrate improved immunogenicity are set forth below. A more detailed description of the GBS antigens referred to in these experiments is set forth following the examples.

Example 1

Active Maternal Immunization Assay of GBS 80 Alone vs. in Combination

In this example, the Active Maternal Immunization Assay was used to measure the percent survival of pups challenged with a Type III serotype of GBS (COH1 isolate), at t=56 days. The maternal mice were immunized according to the Active Maternal Immunization Assay schedule discussed above with GBS 80 alone, combinations of GBS antigens (with and without GBS 80), placebo (PBS) or inactivated whole cell

GBS isolate as indicated in Table 3 below. In these experiments, the challenge dose for GBS Type III, strain isolate COH1 sufficient to kill 70-90% of unimmunized pups is approximately equal to 10xLD 50% (where LD 50% is the statistically derived Median Lethal Dose).

TABLE 3

Active Maternal Immunization Assay of GBS 80 alone vs. in combination		
I Challenge t = 56 days Type III COH1 10 x LD 50%		
α -GBS	Alive/treated	Survival %
α -PBS	3/26	11
α -GBS III	9/20	45
80	24/34	70
80 + 338 + 330	39/40	97
80 + 330 + 104	38/40	95
80 + 104 + 404	24/24	100
80 + 338 + 104	33/34	97
80 + 338 + 404	30/30	100
338 + 330 + 104	22/30	73
338 + 104 + 404	24/37	65
80 + 330 + 404	25/28	89

As shown in Table 3, combinations of GBS antigens which included GBS 80 demonstrated an improved immunogenicity over the use of the antigens alone. For example, immunization with GBS 80 alone yielded a 70% survival rate among the challenged pups. Immunization with combinations of GBS 80 with GBS 338, GBS 330, GBS 104, and GBS 404 yielded 95 to 100% survival rate among the challenged pups. This is an increase of 25 to 30 percentage points.

By comparison, combinations of these antigens which did not include GBS 80 failed to achieve the % survival of GBS 80 alone. For example, immunization with GBS 338, GBS 104 and GBS 404 yielded a 65% survival rate. Replacement of any one of these antigens with GBS 80 dramatically increased the percent survival rate to between 97 and 100%. This is an increase of 32 to 35 percentage points. (See percent survival rates of GBS 80, 338, 101(97%); GBS 80, 338, 404 (100%) and GBS 80, 104, 404 (100%)). Similarly, immunization with GBS 338, 330 and 104 yielded a 73% survival rate. Replacement of any one of these antigens with GBS 80 increased the percent survival rate to between 95-97%.

These findings indicate that protection from COH1 isolate is increased with use of GBS 80 in combination with other GBS antigens.

Example 2

Active Maternal Immunization Assay of GBS 80, GBS 322 GBS 276, GBS 104 Alone vs. in Combination

In this example, the Active Maternal Immunization Assay was used to measure the percent survival of pups challenged with a Type III serotype of GBS (COH1 isolate) at t=56 days. The maternal mice were immunized according to the Active Maternal Immunization Assay schedule discussed above with a single GBS antigen, combinations of GBS antigens with GBS 80, and placebo (PBS) as indicated in Table 4 below.

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TABLE 4

Active Maternal Immunization Assay of GBS 80, GBS 322, GBS 276 or GBS 104 alone vs. in combination with GBS 80		
I Challenge t = 56 days Type III COH1 10 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 322 + 104	27/27	100
80 + 322 + 276	35/38	92
80 + 322 + 91	24/24	100
80 + 104 + 276	29/30	97
80 + 104 + 91	36/40	90
80 + 276 + 91	33/40	82
GBS 80	24/30	80
GBS 322	7/40	17
GBS 276	13/37	35
GBS 104	28/38	74
α-PBS	2/27	7

As shown in Table 4, the combinations of the antigens with GBS 80 yielded improved immunogenicity over the use of the antigens alone. For example, immunization with GBS 322 alone yielded a 17% survival rate among the challenged pups. Immunization with combinations of GBS 322 with GBS 80 and another GBS antigen yielded survival rates of 92-100%. As another example, immunization with GBS 104 alone yielded a 74% survival rate. Immunization with combinations of GBS 104 with GBS 80 and another GBS antigen yielded survival rates of 90-100%. As another example, immunization with GBS 276 alone yielded a 35% survival rate. Immunization with combinations of GBS 276 with GBS 80 and another GBS antigen yielded survival rates of 82-97%.

Having demonstrated the immunogenicity of the above-described combinations, the duration of the immune response in the mouse model was further analysed. The maternal mice used in the above described Active Maternal Immunization Assay were mated a second time and the resulting pups challenged with a different GBS serotype (Type V, CJB 111 isolate) at a dramatically higher dose (300×LD 50%) at t91 days. The parameters of this second, much stronger challenge were outside those of the standard Active Maternal immunization Assay and were meant to probe the limits of the immunological memory generated from the original maternal immunization in the mouse model. Indication of immunological memory in this model under these conditions is thought to be significant. As shown in Table 5, even under these extreme conditions, increased survival rates were generally achieved, particularly for the combination comprising GBS 80, GBS 322 and GBS 104. It was surprising to note that the percent survival rate for the combination of GBS 80, GBS 233 and GBS 104 was 100% for both the first and second challenges.

TABLE 5

Second generation pups challenged with higher dose of different strain		
II Challenge t = 91 days Type V CJB111 300 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 322 + 104	20/20	100
80 + 322 + 276	32/37	86
80 + 322 + 91	27/30	90
80 + 104 + 276	22/37	59
80 + 104 + 91	36/39	92

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TABLE 5-continued

Second generation pups challenged with higher dose of different strain		
II Challenge t = 91 days Type V CJB111 300 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 276 + 91	23/28	82
GBS 80	13/30	43
GBS 322	25/30	83
GBS 276	18/40	45
GBS 104	21/39	54
α-PBS	9/36	25

Example 3

Active Maternal Immunization Assay of combinations of GBS 80 with GBS 690, GBS 691, GBS 338, GBS 305, GBS 361 and GBS 184

In this example additional combinations of GBS antigens were used in the Active Maternal Immunization Assay, again with a GBS Type III COH1 isolate challenge. The maternal mice were immunized according to the Active Maternal Immunization Assay schedule described above with the combinations of GBS antigens set forth in Table 6 below.

TABLE 6

Active Maternal Immunization Assay using combinations of GBS 80 with GBS 690, GBS 691, GBS 338, GBS 305, GBS 361 and GBS 184		
I Challenge t = 56 days Type III COH1 10 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 690 + 691	26/29	90
80 + 690 + 338	35/40	87
80 + 690 + 305	34/35	97
80 + 691 + 305	37/40	92
80 + 338 + 305	25/30	83
80 + 338 + 361	26/30	87
80 + 305 + 361	23/30	77
80 + 184 + 691	32/39	82
α-PBS	10/40	25

The maternal mice in this model were also mated a second time and the resulting pups challenged with the same GBS isolate at a dramatically higher dose (100×LD 50%) at t=84 days. As in the example above, the parameters of this second, much stronger challenge were outside those of the standard Active Maternal Immunization Assay and were meant to probe the limits of the immunological memory generated from the original maternal immunization in the mouse model. As shown in Table 7, even under these extreme conditions, some of the survival rates remained at or above 70%. Surprisingly, the percent survival rates for the combination of GBS 80, GBS 184 and GBS 691 actually increased.

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TABLE 7

Second generation pups challenged with higher dose		
II Challenge t = 84 days Type III COH1 100 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 690 + 691	19/39	49
80 + 690 + 338	21/30	70
80 + 690 + 305	23/40	57
80 + 691 + 305	22/30	73
80 + 338 + 305	18/30	60
80 + 338 + 361	25/40	62
80 + 305 + 361	21/30	70
80 + 184 + 691	35/40	87
α-PBS	4/20	20

Example 4

Active Maternal Immunization Assay using combinations of GBS 80 with GBS 690, GBS 691, GBS 338, GBS 305, and GBS 361

In this example additional combinations of GBS antigens were used in the Active Maternal Immunization Assay, this time with a GBS Type V, CJB111 isolate challenge. In these experiments, the challenge dose for the GBS Type V, CJB111 isolate sufficient to kill 70-90% of unimmunized pups is approximately equal to 60×LD 50% (where LD 50% is the statistically derived Median Lethal Dose). The maternal mice were immunized according to the Active Maternal Immunization Assay schedule described above with the combinations of GBS antigens set forth in Table 8 below. As shown in Table 8, in this particular challenge study with this specific Type V strain isolate, the survival rates for all of the combinations achieved at least 70%.

TABLE 8

Active Maternal Immunization Assay using combinations of GBS 80 with GBS 690, GBS 691, GBS 338, GBS 305 and GBS 361		
I Challenge t = 56 days Type V CJB111 60 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 690 + 691	24/30	80
80 + 690 + 338	11/17	70
80 + 691 + 338	7/10	70
80 + 691 + 305	21/30	70
80 + 338 + 305	26/30	87
80 + 338 + 361	26/30	87
80 + 305 + 361	28/30	93
GBS 80	21/30	70
α-PBS	5/18	28

The maternal mice in this model were also mated a second time and the resulting pups challenged with the same GBS isolate at a dramatically higher dose (600×LD 50%) at t=84 days. As in the example above, the parameters of this second, much stronger challenge were outside those of the standard Active Maternal Immunization Assay and were meant to probe the limits of the immunological memory generated from the original maternal immunization in the mouse model. As shown in Table 9, even under these extreme conditions, some of the survival rates remained above 70%. Surprisingly, the percent survival for two of the antigen groups actually increased (GBS 80, GBS 690 and GBS 338) and (GBS 80, GBS 691 and GBS 338).

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TABLE 9

Second generation pups challenged with higher dose		
II Challenge t = 84 days Type V CJB111 600 × LD 50%		
α-GBS	Alive/treated	Survival %
80 + 690 + 691	27/37	73
80 + 690 + 338	15/20	75
80 + 691 + 338	27/30	90
80 + 691 + 305	23/40	57
80 + 338 + 305	12/20	60
80 + 338 + 361	24/30	80
80 + 305 + 361	24/30	80
GBS 80	24/30	80
α-PBS	ND	ND

Example 5

Active Maternal Immunization Assay using Combinations of GBS 80 with GBS 104, GBS 276, and GBS 322

In this example an additional combination of GBS antigens was used in the Active Maternal Immunization Assay, this time with an isolate challenge of different GBS strains. In these experiments, the challenge dose for the different GBS strains was sufficient to kill 60-90% of unimmunized pups and is equal to 10×LD 50% (where LD 50% is the statistically derived Median Lethal Dose). The maternal mice were immunized according to the Active Maternal Immunization Assay schedule described above with the combination of GBS 80 antigen with GBS 104, GBS 276, and GBS 322 antigens in the GBS strains set forth in Table 10 below. Survival % was observed with the GBS combination with two different adjuvants, Alum and Freund's. As shown in Tables 10 and 11, in this particular challenge study, the survival rates for the combination in all of the GBS strains achieved up to 96%.

TABLE 10

Active Maternal Immunization Assay using combinations of GBS 80 with GBS 104, GBS 276, and GBS 322 - Alum adjuvant					
ALUM				PBS	
Mix = 322 + 80 + 104 + 276				Alive/ treated	Survival %
GBS strains	Type	Alive/treated	Survival %		
JM9130013	VIII	32/36	89	18/46	40
CJB111	V	118/145	81	21/110	19
COH1	III	96/115	83	22/104	21
M781	III	42/52	81	18/48	38
2603	V	79/145	54	28/128	22
18RS21	II	86/186	46	24/131	18
DK21	II	31/140	22	28/118	24
7357b-	Ib	25/88	28	25/106	23
A909	Ia	4/40	10	9/60	15
090	Ia	2/31	6	4/53	7
SMO53	VII	17/54	31	4/39	10

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TABLE 11

Active Maternal Immunization Assay using combinations of GBS 80 with GBS 104, GBS 276, and GBS 322 - Freund adjuvant Freund					
				PBS	
Mix = 322 + 80 + 104 + 276				Alive/ treated	Survival %
GBS strains	Type	Alive/treated	Survival %		
JM9130013	VIII	nd	nd	nd	nd
CJB111	V	47/49	96	12/46	26
COH1	III	47/50	94	12/50	24
M781	III	33/50	66	6/50	12
2603	V	28/30	93	8/48	17
18RS21	II	31/78	40	10/46	22
DK21	II	37/68	54	15/60	25
H36B	Ib	8/38	21	5/60	8
7357b-	Ib	29/50	58	5/50	10
A909	Ia	18/49	37	6/49	12

Accordingly, the invention therefore includes compositions comprising combinations of two or more GBS antigens, wherein the combination includes GBS 80 or a fragment thereof or a polypeptide sequence having sequence identity thereto.

In one embodiment, the combination may consist of two to thirteen GBS antigens, including GBS 80. As an example, the combination may contain GBS 80 and other GBS antigens selected from the group consisting of GBS 80, GBS 91, GBS 104, GBS 184, GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361, GBS 404, GBS 690, and GBS 691. Preferably, the combination includes GBS 80 in combination with one or more of GBS 104 and GBS 322. For example, the combination may include GBS 80, GBS 104, GBS 322 and GBS 67.

Instead of the full length antigen, the combination may comprise an immunogenic fragment of the selected GBS antigen and/or a polypeptide sequence having sequence identity to the selected antigen.

Preferably, the combination of GBS antigens consists of three, four, five, six, seven, eight, nine, or ten GBS antigens. Still more preferably, the combination of GBS antigens consists of three, four, or five GBS antigens.

Details of examples of GBS antigens for use in combination with GBS 80 are set forth below.

GBS 91
GBS 91 refers to a GBS C3 binding polypeptide. Nucleotide and amino acid sequences of GBS 91 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8937 and SEQ ID 8938. These sequences are set forth below as SEQ ID NOS 10 and 11:

SEQ ID NO. 10
ATGAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAA
ATATAAATTTGGTTTAGCATCAGTAATTTAGGGTCATTCATAATGGTCA
CAAGTCCTGTTTTGCGGATCAAACATACATCGGTTCAAGTTAATAATCAG
ACAGGCACTAGTGTGGATGCTAATAATCTTCCATGAGACAAGTGCCTC
AAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATAAAGTTG
TAAATAGTCAAAATACGGCAACAAGGACATTACTACTCTTTAGTAGAG
ACAAAGCCAATGGTGGAAAAACATTACCTGAACAAGGAATTATGTTTA
TAGCAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAG
CTTCTATGCAAGAAAGGTGATAAAGTTTTCTATGACCAAGTATTTAAT

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-continued

AAAGATAATGTGAAATGGATTTTCATATAAGTCTTTTTGTGGCGTACGTCG
ATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTGAGAGACTAAAG
5 CACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAGAAAATAGCA
ACGCAAGGAAATTATACATTTTCACATAAAGTAGAAGTAAAAATGAAGC
TAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGACAGAATTT
10 TTTACGACCAATACTAATACTATTGAAGGAAATCAGTGGTTATCTTATAAA
TCATTCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGCATCTTCAGT
AGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCACAAGCCCGTA
15 TTACTAAAAGTGGTAGACTGACTATTTCTAACGAAACAACTACAGGTTTT
GATATTTTAAATTACGAATATTAAGATGATAACGGTATCGTCTGTGTTAA
GGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTAATGGTATA
20 CAGCTGTAATACTACTGGGGATGGCAACTACAAGTAGCTGTATCATTTGCT
GACCATAAGAATGAGAAGGGTCTTTATAATATTCAATTTATACCTACCAAGA
AGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTGACAGTAGCTG
25 GAACTAATCTCTCAAGAACCTATTGAAATGGTTTAGCAAAGACTGGT
GTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATC
AAGTCAGACCCAATTTACTTTAGAAAAAGGTGACAAAATAAATTATGATC
30 AAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGT
GGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAGTAGTGAAAA
AGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTACCTAAAA
35 CAGGTACCTATACATTACTAAAAGTGTAGATGTGAAAAGTCAACCTAAA
GTATCAAGTCCAGTGAATTTAATTTTCAAAAGGGTGAAAAATACATTA
TGATCAAGTGTAGTAGTAGATGGTCATCAGTGATTTTCATACAAGAGTT
40 ATTCCGGTATTCGTCGCTATATTGAAATT
SEQ ID NO. 11
MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSVPFADQTTTSVQVNNQ
45 TGTSVDANNSSNETSASSVITSNNDSVQASDKVNSQNTATKIDITPLVE
TKPMVEKLTPEQGNVYVSKETEVKNTPSKSPVAFYAKKGDKVFYDQVFN
KDNVWKWISYKSPCGVRRYAAIESLDPSGGSETKAPTPTVNSGSNNQEKIA
TQGNVTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIENQWLSYK
50 SFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGF
DILITNKKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNQKVAVSFA
55 DHKNEKGLYNIHLYYQEASGTLVGVTGKTVAGTNSSQEPIENGLAKTG
VYNIIGSTEVKNEAKISSQTQFTLEKDKINYDQVLADGYQWISYKSYK
GVRRIYPVKLLTSSEKAKDEATKPTSPNLPKTGTYYTFTKTVDVKSQPK
60 VSSPVFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYIEI

GBS 91 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 11 above. In one embodiment, one or more amino acids from this leader or signal sequence region of GBS 91 are removed. An example of such a GBS 91 fragment is set forth below as SEQ ID NO: 12.

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SEQ ID NO: 12
 DQTTSVQVNNQTGTSVDANNSSNETSASSVITSNNDSVQASDKVNSQNT
 ATKDITTLPLVETKPMVEKTLPEQGNVYVSKETEVKNTPSKAPVAFYAKK
 GDKVFDQVFNKDNVWISYKFCGVRRYAAIESLDPSGGSETKAPTPTVT
 NSGSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQIL
 TIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGR
 LTISNETTTGFDILITNKKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTG
 DGNVYKAVSFADHKNEKGLYNIHLYYQIASGTLVGVGTGKTVAGTNSSQ
 EPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINYDQVLTAD
 GYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYNLPKGTGTYTF
 TKTVDVKSQPKVSSPVEFNQKGEKIHVDQVLVDGHQWISYKSYSGIRR
 YIEI

GBS 91 contains a C-terminal transmembrane region which may be located within the underlined region near the end of SEQ ID NO: 11 above. In one embodiment, one or more amino acids from the transmembrane and cytoplasmic regions are removed. An example of such a GBS 91 fragment is set forth below as SEQ ID NO: 13.

SEQ ID NO: 13
 MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPVFADQTTSVQVNNQ
 TGTSVDANNSSNETSASSVITSNNDSVQASDKVNSQNTATKDITTLPLVE
 TKPMVEKTLPEQGNVYVSKETEVKNTPSKAPVAFYAKKGDKVFDQVFN
 KDNVWISYKFCGVRRYAAIESLDPSGGSETKAPTPTVNSGSNNQEKIA
 TQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYK
 SFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTG
 DILITNKKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFA
 DHKNEKGLYNIHLYYQIASGTLVGVGTGKTVAGTNSSQEPHENGLAKTG
 VYNIIGSTEVEKNEAKISSQTQFTLEKGDKINYDQVLTADGYQWISYKSYSG
 VRRYIPVKKLTTSSSEKAKDEATKPTSYNLPKGTG

GBS 91 contains an amino acid motif indicative of a cell wall anchor: SEQ ID NO: 14 LTKTG (shown in *italics* in SEQ ID NO: 11 above). In one embodiment, both the transmembrane domain and the cell wall anchor motif are removed from GBS 91. An example of such a GBS 91 fragment is set forth below as SEQ ID NO: 15.

SEQ ID NO: 15
 MKKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSPVFADQTTSVQVNNQ
 TGTSVDANNSSNETSASSVITSNNDSVQASDKVNSQNTATKDITTLPLVE
 TKPMVEKTLPEQGNVYVSKETEVKNTPSKAPVAFYAKKGDKVFDQVFN
 KDNVWISYKFCGVRRYAAIESLDPSGGSETKAPTPTVNSGSNNQEKIA
 TQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYK
 SFNGVRRFVLLGKASSVEDTEDKEKVSPPQARITKTGRLTISNETTTG
 DILITNKKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDNVYKAVSFA
 DHKNEKGLYNIHLYYQIASGTLVGVGTGKTVAGTNSSQEPHENGLAKTG

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VYNIIGSTEVEKNEAKISSQTQFTLEKGDKINYDQVLTADGYQWISYKSYSG
 VRRYIPVKKLTTSSSEKAKDEATKPTSYN

5 In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane and cytoplasmic regions are removed from the GBS 91 sequence. An example of such a GBS 91 fragment is set forth below as SEQ ID NO: 16.

10
 SEQ ID NO: 16
 DQTTSVQVNNQTGTSVDANNSSNETSASSVITSNNDSVQASDKVNSQNT
 ATKDITTLPLVETKPMVEKTLPEQGNVYVSKETEVKNTPSKAPVAFYAKK
 15 GDKVFDQVFNKDNVWISYKFCGVRRYAAIESLDPSGGSETKAPTPTVT
 NSGSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQIL
 TIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGR
 20 LTISUETTGTGFDILITNKKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTG
 DGNVYKAVSFADHKNEKGLYNIHLYYQIASGTLVGVGTGKTVAGTNSSQ
 EPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINYDQVLTAD
 25 GYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYNLPKGTG

In another embodiment, the leader or signal sequence region, the transmembrane and cytoplasmic regions, and the cell wall anchor motif are all removed from the GBS 91 sequence. An example of such a GBS 91 fragment is set forth below as SEQ ID NO: 17.

SEQ ID NO: 17
 35 DQTTSVQVNNQTGTSVDANNSSNETSASSVITSNNDSVQASDKVNSQNT
 ATKDITTLPLVETKPMVEKTLPEQGNVYVSKETEVKNTPSKAPVAFYAKK
 GDKVFDQVFNKDNVWISYKFCGVRRYAAIESLDPSGGSETKAPTPTVT
 40 NSGSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQIL
 TIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGR
 LTISNETTTGFDILITNKKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTG
 45 DGNVYKAVSFADHKNEKGLYNIHLYYQIASGTLVGVGTGKTVAGTNSSQ
 EPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINYDQVLTAD
 GYQWISYKSYSGVRRYIPVKKLTTSSSEKAKDEATKPTSYN

50 Further information regarding GBS 91 can be found in WO 01/25440 (C3 binding polypeptide), WO 01/32882 (ID-65), WO 02/31156 (BVH) and Reinscheid et al., *Microbiology* (2002) 148: 3245-3254 (bsp gene), each of which are incorporated herein by reference in their entirety.

55 GBS 104

GBS 104 refers to a putative cell wall surface anchor family protein. It has been referred to as emaA protein. Nucleotide and amino acid sequences of GBS 104 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8777 and SEQ ID 8778. These sequences are set forth below as SEQ ID NOS 18 and 19:

SEQ ID NO: 18
 65 ATGAAAAAGAGACAAAAATATGGAGAGGGTTATCAGTTACTTTACTAAT
 CCTGTCCCAATTCCATTGGTATATTGGTACAGGTGAACCAAGATA

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CCAATCAAGCACTTGGAAAAGTAATTGTTAAAAAACGGGAGACAATGCT
 ACACCATTAGGCAAAGCGACTTTTGTGTTAAAAATGACAATGATAAGTC
 AGAAACAAGTCACGAAACGGTAGAGGGTTCGAGAGAAGCAACCTTTGAAA
 ACATAAAACCTGGAGACTACACATTAAGAGAAGAAACAGCACCAATTGGT
 TATAAAAAAAGCTGATAAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGC
 AACATAATCGAGGGTATGGATGCAGATAAAGCAGAGAAACGAAAGAAG
 TTTTGAATGCCCAATATCCAAATCAGCTATTTATGAGGATACAAAAGAA
 AATTACCCATTAGTTAATGTAGAGGGTCCAAAGTTGGTGAACAATACAA
 AGCATTGAATCCAATAAATGGAAAAGATGGTCAAGAGAGATTGCTGAAG
 GTTGGTTATCAAAAAAATTACAGGGGTCAATGATCTCGATAAGAATAAA
 TATAAAATTGAATTAAGTGTGAGGGTAAACCACTGTTGAAACGAAAGA
 ACTTAATCAACCACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTA
 TGAATAATGAAAGAGCCAATAATCTCAAAGAGCATTAAAGCTGGGGAA
 GCAGTTGAAAAGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGT
 AGCTCTGTGACATATGCCTCAACCATTTTTGATGGTACTGAAGCGACCG
 TATCAAAGGGAGTTGCCGATCAAATGGTAAAGCGCTGAATGATAGTGTA
 TCATGGGATTATCATAAACTACTTTTACAGCAACTACACATAATTACAG
 TTATTTAAATTTAACAATGATGCTAACGAAGTTAATATTCTAAAGTCAA
 GAATTCCAAAGGAAGCGAGCATATAATGGGGATCGCACGCTCTATCAA
 TTTGGTGCACATTTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTT
 AGAGACACAAAGTTCTAATGCTAGAAAAAAGCTTATTTTACGTAAGT
 ATGGTGTCCCTACGATGCTTATGCCATAAATTTAATCCTTATATATCA
 ACATCTTACCAAAACCAAGTTTAATTTCTTTTAAATAAAATACCAGATAG
 AAGTGGTATTCTCCAAGAGGATTTTATAATCAATGGTATGATTATCAA
 TAGTAAAGGAGATGGAGAGAGTTTAAACTGTTTTCGGATAGAAAAGTT
 CCTGTACTGGAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCA
 ACTCTCTGTAATGAGTAATGAGGGATATGCAATTAATAGTGGATATATTT
 ATCTCTATTGGAGAGATTACAACGGGTCTATCCATTGATCCTAAGACA
 AAGAAAGTTTCTGCAACGAAACAAATCAAACTCATGGTGAGCCAACAAC
 ATTATACCTTAATGGAATATAAGACCTAAAGGTTATGACATTTTACTG
 TTGGGATTGGTGTAACGAGATCCTGGTGCAACTCCTCTGAAGCTGAG
 AAATTTATGCAATCAATATCAAGTAAACAGAAAAATTATACTAATGTTGA
 TGATACAAATAAAATTTATGATGAGCTAAATAAATACTTTAAACAATTG
 TTGAGGAAAAACATTCTATTGTTGATGGAATGTGACTGATCCATGGGA
 GAGATGATTGAATCCAATTAATAAATGGTCAAAGTTTACACATGATGA
 TTACGTTTTGGTTGGAATGATGCGAGTCAATTAATAAATGGTGTGGCTC
 TTGGTGGACCAACAGTGATGGGGGAATTTTAAAGATGTTACAGTGACT
 TATGATAAGACATCTCAAACCATCAAATCAATCATTTGAAGTTAGGAAG
 TGGACAAAAAGTAGTTCTTACCTATGATGTACGTTTAAAGATAACTATA
 TAAGTAACAAATTTTACAATACAAATAATCGTACAACGCTAAGTCCGAAG

20

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AGTGAAAAAGAACCAATACTATTCTGTGATTTCCCAATCCCAAAATTCG
 TGATGTTCTGTGAGTTTCCGGTACTAACCATCAGTAATCAGAAGAAAAATGG
 5 GTGAGGTTGAATTTATTAAGTTAATAAAGACAAACATTGAGAAATCGCTT
 TTGGGAGCTAAGTTTCACTTCAAGATAGAAAAAGATTTTCTGGGTATAA
 GCAATTTGTTCCAGAGGGAAGTGATGTTACAACAAAGAAATGATGGTAAAA
 10 TTTATTTTAAAGCACTTCAAGATGGTAACTATAAATTATATGAAATTTCA
 AGTCCAGATGGCTATATAGAGGTAAAAACGAAACCTGTTGTGACATTTAC
 AATTCAAATGGAGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATA
 15 AAAATCAAATCGGGTATCTTGAAGGAAATGGTAAACATCTTATTACCAAC
 ACTCCCAACGCCACCAGGTGTTTTCTCTAAACAGGGGGAATTGGTAC
 AATTGCTATATATTAGTTGGTCTACTTTTATGATACTTACCATTGTT
 CTTTCCGTCGTAAACAATTG
 20
 SEQ ID NO. 19
MKKRQKIWRGLSVTLILLSQIPFGILVQGETQDTNQALGKIVKKTGDNA
 TPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPGDYTLREETAPIG
 25 YKKTDKTWKVKVADNGATIIEGMDADKAEKRKEVLNAQYPKSAIYEDTKE
 NYPLVNEGSKVGEQYKALNPINGKDGREEIAEGWLSKKITGVNDLDKKN
 YKIELTVEGKTTVETKELNQPLDVVLLDNSNSMNNERANNSQRALKAGE
 30 AVEKLIDKITSNKDNRVALVTYASTIFDGTEATVSKGVADQNGKALNDSV
 SWDYHKTTFTATTHNYSYLNLTNDANEVNLKSRIPKEAEHINGDRTLYQ
 FGATFTQKALMKANEILETQSSNARKKLIFHVTGVPMTSYAINFNPIYIS
 35 TSYQNQFNSFLNKIPDRSGILQEDFIINGDDYQIVKGDGESFKLFSDRKV
 PVTGGTTQAAAYRVPQNQLSVMSNEGYAINSGLYLYWRDYNWVYFPDPKT
 KKVSAKQIKTHGEPTTLYFNGNIRPKGYDIFTVGIVNGDPGATPLEAE
 40 KFMQSISSKTENYTNVDDTNKIYDELNKYFDTIVEEKHSIVDGNVTPMG
 EMIEFQLKNGQSFTHDDYVLVNGDGSQKNGVALGGPNSDGGILKDVTVT
 YDKTSQTIKINHLNLGSGQKVVLTYDVRKLDNYISNKFYNTNNRTTSLPK
 SEKEPNTIRDFPIPKIRDVREFPVLTISNQKKMEGEVFIKVNKDKHSESL
 45 LGAKFQLQIEKDFSGYKQFVPEGSDVTTKNDGKIYFKALQDGNKYLYEIS
 SPDGYIEVKTKPVVTFITQNGEVNTLKDAPNANKNQIGYLENGKHLITN
TPKRPPGVFPKTTGGIGTIVYILVGSFTMILTICSFRKQL

50 GBS 104 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO 19 above. In one embodiment, one or more amino acid sequences from the leader or signal sequence region of GBS 104 are removed. An example of such a GBS 104 fragment is set forth below as SEQ ID NO 20.

SEQ ID NO 20
 60 GETQDTNQALGKIVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSG
 EATFENIKPGDYTLREETAPIGYKKTDKTWKVKVADNGATIIEGMDADKA
 EKRKEVLNAQYPKSAIYEDTKENYPLVNEGSKVGEQYKALNPINGKDR
 REIAEGWLSKKITGVNDLDKKNYKIELTVEGKTTVETKELNQPLDVVLL
 65 DNSNSMNNERANNSQRALKAGEAVEKLIDKITSNKDNRVALVTYASTIFD

21

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GTEATVSKGVADQNGKALNDSVSWDYHKTTFATTTHNYSYLNLTNDANEV
 NILKSRIPKEAEHINGDRTLYQFGATFTQKALMKANEILETQSSNARKKL
 IFHVTGVPMTSYAINFNPIYSTSYQNQFNSFLNKIPDRSGILQEDFIIN
 GDDYQIVKGDGESFKLFSRDKVPVTGGTTQAAAYRVPQNQLSVMSNEGAYAI
 NSGYIYLYWRDYNWVYFPDPKTKKVSATKQIKTHGEPTTLYFNGNIRPKG
 YDIFTVGIGVNGDPGATPLEAEKFMQSISSTENYTNVDDTNKIYDELNK
 YFKTIVEEKHSIVDGNVTDPMGEMIEFQKNGQSFTHDDYVLVNGDGSQ
 KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVLTVDVR
 LKDNYSISNKFYNTNNRTTSLPKSEKEPNTIRDFFIPKIRDVREFFVLTIS
 NQKKMGEVEFIKVNKDKHSESLGAKFQLQIEKDFSGYKQFVPEGSVDTT
 KNDGKIYFKALQDGNKYLYEISSPDGYIEVKTKPVVTFTIQNGEVTNLKA
 DPNANKNQIGYLEGNGKHLITNTPKRPPGVFPKGGIGTIVYILVGSFTM
 ILTICSPRRKQL

GBS 104 contains a C-terminal transmembrane and/or cytoplasmic region which is indicated by the underlined region near the end of SEQ ID NO 19 above. In one embodiment, one or more amino acids from the transmembrane or cytoplasmic regions are removed. An example of such a GBS 104 fragment is set forth below as SEQ ID NO 21.

SEQ ID NO: 21
 MKKRQKIWRGLSVTLILLSQIPFGILVQGETQDTNQALGKVIKKTGDNA
 TPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPGDYTLREETAPIG
 YKKTDKTWKVKVADNGATIIEGMDADKAERKEVLNAQYPKSAIYEDTKE
 NYPLVNVVEGSKVGEQYKALNPINGKDGREIAEGWLSKKITGVNDLDKNK
 YKIELTVEGKTTVETKELNQPLDVVLLDNSNSMNNERANNSQRALKAGE
 AVEKLIDKITSNKDNVALVTYASTIFDGTATVSKGVADQNGKALNDSV
 SWDYHKTTFATTTHNYSYLNLTNDANEVNILKSRIPKEAEHINGDRTLYQ
 FGATFTQKALMKANEILETQSSNARKKLIFHVTGVPMTSYAINFNPIYIS
 TSYQNQFNSFLNKIPDRSGILQEDFIINGDDYQIVKGDGESFKLFSRDKV
 PVTGGTTQAAAYRVPQNQLSVMSNEGAYAINSGYIYLYWRDYNWVYFPDPKT
 KVSATKQIKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAE
 KFMQSISSTENYTNVDDTNKIYDELNKYFKTIVEEKHSIVDGNVTDPMG
 EMIEFQKNGQSFTHDDYVLVNGDGSQKNGVALGGPNSDGGILKDVTVT
 YDKTSQTIKINHLNLGSGQKVLTVDVRLKDNYSISNKFYNTNNRTTSLPK
 SEKEPNTIRDFFIPKIRDVREFFVLTISNQKKMGEVEFIKVNKDKHSESL
 LGAKFQLQIEKDFSGYKQFVPEGSVDTTKNDGKIYFKALQDGNKYLYEIS
 SPDGYIEVKTKPVVTFTIQNGEVTNLKADPNANKNQIGYLEGNGKHLITN
 T

In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic regions are removed. An example of such a GBS 104 fragment is set forth below as SEQ ID NO 22.

22

SEQ ID NO: 22

GETQDTNQALGKVIKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSG
 EATFENIKPGDYTLREETAPIGYKKTDKTWKVKVADNGATIIEGMDADKA
 5 EKRKEVLNAQYPKSAIYEDTKENYPLVNVVEGSKVGEQYKALNPINGKDG
 REIAEGWLSKKITGVNDLDKNKYKIELTVEGKTTVETKELNQPLDVVLL
 DNSNSMNNERANNSQRALKAGEAVEKLIDKITSNKDNVALVTYALTIFD
 10 GTEATVSKGVADQNGKALNDSVSWDYHKTTFATTTHNYSYLNLTNDANEV
 NILKSRIPKEAEHINGDRTLYQFGATGTQKALMKANEILETQSSNARKKL
 IFHVTGVPMTSYAINFNPIYSTSYQNQFNSFLNKIPDRSGILQEDFIIN
 15 GDDYQIVKGDGESFKLFSRDKVPVTGGTTQAAAYRVPQNQLSVMSNEGAYAI
 NSGYIYLYWRDYNWVYFPDPKTKKVSATKQIKTHGEPTTLYFNGNIRPKG
 YDIFTVGIGVNGDPGATPLEAEKFMQSISSTENYTNVDDTNKIYDELNK
 20 YFKTIVEEKHSIVDGNVTDPMGEMIEFQKNGQSFTHDDYVLVNGDGSQ
 KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVLTVDVR
 LKCNYSISNKFYNTNNRTTSLPKSEKEPNTIRDFFIPKIRDVREFFVLTIS
 25 NQKKMGEVEFIKVNKDKHSESLGAKFQLQIEKDFSGYKQFVPEGSVDTT
 KNDGKIYFKALQDGNKYLYEISSPDGYIEVKTKPVVTFTIQNGEVTNLKA
 DPNANKNQIGYLEGNGKHLITNT

30 In other embodiments, additional fragments of GBS 104 are provided including an 830 amino acid fragment of GBS 104 of amino acids 28-858, a 359 amino acid fragment of GBS 104 of amino acids 28-387, a 581 amino acid fragment of GBS 104 of amino acids 28-609, or a 740 amino acid fragment of GBS 104 of amino acids 28-768.

GBS 184

GBS 184 refers to a putative lipoprotein. Nucleotide and amino acid sequences of GBS 184 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 1977 and SEQ ID 1978. These sequences are also set forth below as SEQ ID NOS 23 and 24.

SEQ ID NO: 23
 45 ATGAAAAACAAAACTATTACTGCTTATTGGAGGCTTATTAATAATGAT
 AATGATGACAGCATGTAAGGATTCAAAATCCAGAAAAACCGACAAAGG
 AAGAGTACCAAGCTGAACAAAATTTTAAACCGTTTGTGAGTTTGTAGCA
 50 CAAAAAGATAAAGATTGAGCAAAATACAAAAATACTTACTATTAGTATC
 GGATTGAGGTGATGCATTAGATTAGAATATTTCTATAGTATTCAAGATT
 TAAAAAAAATAAGGATTAGGGAAGTTTGAAACAAGAAAAAGTCAAATA
 55 GAAAAGCCGGGTGGCTATAATGAGTTAGAAAAATAAGAGGTCCCATTGTA
 ATATTTTAAAAATAATATAGTTTATCCAAAAGGAAACCGAATATTACAT
 TTGATGACTTTATTATCGGAGCAATGGATACTAAGAATTAAGAATTA
 60 AAAAAATTAAGTAAAGTATTTATTAAAAACATCCGGAACTGAGTT
 GAAAGATATAACATATGAATTGCCGACACAGTCGAAGCTTATTAATAAAA

SEQ ID NO: 24
 65 MKKQKLLLLIGLLIMMTACKDSKIPENRTKEEYQAEQNFKPFPEFLA
 QKDKLSKIQYLLVSDSGDALDLEYFYSIQDLKKNKDLGKFETRKSQI

23

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EKPGGYNELENKEVPFEYFKNNIVYPKGKPNITFDDFIIGAMDTKELKEL
KKLKVKSYLLKHPETELKDITYELPTQSKLIKK

GBS 184 contains a N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO 24, above. In one embodiment, one or more amino acids from the leader or signal sequence are removed from GBS 184. An example of such a GBS 184 fragment is set forth below as SEQ ID NO: 25.

SEQ ID NO: 25

KDSKIPENRTKEEYQAEQNFKPFPEFLAQDKDLSKIQKYLKLVSDSGDA

LDLEYFYISIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFEYFKNN

IVYPKGKPNITFDDFIIGAMDTKELKELKKLVKSYLLKHPETELKDITY

ELPTQSKLIKK

GBS 276

GBS 276 refers to a C5a peptidase. Nucleotide and amino acid sequences of GBS 276 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8941 and SEQ ID 8942. These sequences are set forth below as SEQ ID NOS 26 and 27:

SEQ ID NO: 26

TTGCGTAAAAACAAAACTACCATTTGATAAACTTGCGCTTAT

ATCTACGAGCATCTTGCTCAATGCACAAATCAGACATTAAAGCAAATACTG

TGACAGAAGACACTCTGCTACCGAACAGCCGTAGAACCCCCACAACTCA

ATAGCAGTTTCTGAGGAATCACGATCATCAAGGAACTAAACCTCACA

AACTCCTAGTGATGTAGGAGAAACAGTAGCAGATGACGCTAATGATCTAG

CCCCCTCAAGCTCTGCTAAAACTGCTGATACACAGCAACCTCAAAAGCG

ACTATTAGGGATTGTAACGACCCCTTCTCATGTCAAACCCCTGCAGGAAAA

AGCAGGCAAGGGAGCTGGGACCGTTGTTGCAGTGATTGATGCTGGTTTTG

ATAAAAAATCATGAAGCGTGGCGCTTAACAGACAAAATAAGCAGCTTAC

CAATCAAAAGAAAATCTTGAAAAAGCTAAAAAGAGCACGGTATTACCTA

TGGCGAGTGGGTCAATGATAAGTTGCTTATTACCACGACTATAGTAAAG

ATGGTAAAAACGCTGTTGATCAAGAACACGGCACACAGTGTACAGGATC

TTGTGAGGAAATGCTCCATCTGAAATGAAAGAACCTTACCGCTAGAAAG

TGCGATGCCTGAGGCTCAATTGCTTTTGATGCGTGTGAAATTGTAAATG

GACTAGCAGACTATGCTCGTAACCTACGCTCAAGCTATCAGAGATGCTGTC

AACTTGGGAGCTAAGGTGATTAATATGAGCTTTGGTAATGCTGCACTAGC

TTACGCCAACCTTCCAGACGAAACCAAAAAAGCCTTTGACTATGCCAAAT

CAAAAGGTGTTAGCATTGTGACCTCAGCTGGTAATGATAGTAGCTTTGGG

GGCAAGCCCGTCTACCTCTAGCAGATCATCTGATTATGGGGTGGTTGG

GACACCTGCAGCGGCAGATTCAACATTGACAGTTGCTTCTTACAGCCAG

ATAAACAGCTCACTGAACTGCTACGGTCAAAACAGACGATCATCAAGAT

AAAGAAATGCCTGTTATTATTCAACAAACGCTTTGAGCCAAACAAGGCTTA

CGACTATGCTTATGCTAATCGTGGTACGAAAGAGGATGATTTTAAGGATG

TCGAAGGTAAGATTGCCCTTATTGAACGTGGCGATATTGATTTCAAAGAT

24

-continued

AAGATTGCAAACGCTAAAAAGCTGGTGTGTAGGGGTCTTGATCTATGA

CAATCAAGACAAGGGCTTCCCGATTGAATTGCCAAATGTTGACCAGATGC

CTGCGGCCTTTATCAGTCGAAGAGACGGTCTCTTATAAAGACAATCCC

CCAAAAACCATTACCTTCAATGCGACACCTAAGGTATTGCCAACAGCAAG

TGGCACCAAACTAAGCCGCTTCTCAAGCTGGGGTCTGACAGCTGACGGCA

ATATTAAACCGGATATTGCAGCACCCGCCAAGATATTTTGTATCAGTG

GCTAACACAAGTATGCCAACTTTCTGGAAGTAGTATGCTGCACCATT

GGTAGCGGGTATCATGGGACTGTTGCAAAAGCAATATGAGACACAGTATC

CTGATATGACACCATCAGAGCGTCTTGATTAGCTAAGAAAGATTGATG

AGCTCAGCAACTGCCCTATATGATGAAGATGAAAAAGCTTATTTTCTCC

TCGCCAACAGGGAGCAGGAGCAGTCGATGCTAAAAAGCTTACAGCAGCA

CGATGTATGTAACAGATAAGGACAATACCTCAAGCAAGGTTACCTGAAC

AATGTTTCTGATAAATTTGAAGTAACAGTAACAGTTTCAACAACAACTGTA

TAAACCTCAAGAGTTGTATTACCAAGTAACCTGTTCAAACAGATAAAGTAG

ATGGAACACACTTTGCCTTGGCTCCTAAAGCATTGTATGAGACATCATGG

CAAAAAATCACAATTCCAGCCAATAGCAGCAAAACAGTACCCTTCCAAT

CGATGCTAGTCGATTTAGCAAGGACTTGCTTGCCCCAAATGAAAAATGGCT

ATTTCTTAGAAGGTTTGTTCGTTTCAAACAAGATCCTACAAAAAGAGAG

CTTATGAGCATTCATATATTGGTTTCCGAGGTGATTTTGGCAATCTGTC

AGCCTTAGAAAAACCAATCTATGATAGCAAAGACGGTAGCAGCTACTATC

ATGAAAGCAATAGTGATGCCAAAGACCAATTAGATGGTGATGGATTACAG

TTTTACGCTCTGAAAAATAACTTTACAGCACTTACCACAGAGCTAACCC

ATGGACGATTATTAAAGCTGTCAAAGAAGGGGTTGAAAAATAGAGGATA

TCGAATCTTCAGAGATCAGAGAAACCATTTTTCGAGGTACTTTTGCAAAA

CAAGACGATGATAGCCACTACTATATCCACCGTCACGCTAATGGCAAAAC

ATATGCTGCGATCTCTCCAAATGGGGACGGTAACAGAGATTATGTCCAAT

TCCAAGGTACTTTCTTGCGTAATGCTAAAAACCTTGTGGCTGAAGTCTTG

GACAAAGAAGGAAATGTTGTTTGGACAAGTGAGGTAACCGAGCAAGTTGT

TAAAAACTACAACATGACTTGGCAAGCACACTTGGTTCAACCCGTTTTG

AAAAACGCGTTGGGACGGTAAGATAAAGACGGCAAGTTGTTGCTAAC

GGAACTTACACCTATCGTGTTCGCTACACGCCGATTAGCTCAGGTGCAAA

AGAACAACACACTGATTTTGATGTGATTGTAGACAATACGACACCTGAAG

TCGCAACATCGGCAACATTCTCAACAGAAGATAGTCGTTTGACACTTGCA

TCTAAACCAAAAAACAGCCAACCGGTTTACCGTGAGCGTATTGCTTACAC

TTATATGGATGAGGATCTGCCAACACAGAGTATATTTCTCCAAATGAAG

ATGGTACCTTTACTCTTCTGAGAGGCTGAACAATGGAAGGCGCTACT

GTTCCATTGAAAAATGTCAGACTTTACTTATGTTGTTGAAGATATGGCTGG

TAACATCACTTATACACCAAGTACTAAGCTATTGGAGGGCCACTCTAATA

AGCCAGAACAAGACGGTTCAGATCAAGCACCAGACAAGAAACAGAGCT

AAACCAGAACAAGACGGTTCAGGTCAAACACCAGATAAAAAAAGAAAC

25

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TAAACCAGAAAAAGATAGTTCAGGTCAAACACAGGTAAAACTCCTCAAA
AAGGTCAATCTTCTCGTACTCTAGAGAAACGATCTTCTAAGCGTGCTTTA
GCTACAAAAGCATCAACAAGAGATCAGTTACCAACGACTAATGACAAGGA
TACAAATCGTTTACATCTCCTTAAGTTAGTTATGACCACTTTCTTCTTGG
GA

SEQ ID NO. 27

MRKKQKLPFDKLAIALISTSI LLNAQSDIKANTVTEDTPATEQAVEPPQP
IAVSEESRSSKETKTSQTPSDVGETVADDANDLAPQAPAKTADTPATSKA
TIRDLNDPSHVKTQEKAGKGAGTVVAVIDAGFDKNHEAWRLTDKTKARY
QSKENLEKAKKEHGIYGEWVNDKVAYYHDYSKDGKNAVDQEHGTHVSGI
LSGNAPSEMKEPYRLEGAMPEAQLLLMRVEIVNGLADYARNYAQAIRDAV
NLGAKVINMSFGNAALAYANLPDETCKAFDYAKSKGVSIVTSAGNDSSF
GKPRPLADHPDYGVVGTAAADSTLTVASYSQKQLTETATVKTDDHQD
KEMPVISTNRFEPNKAYDIAYANRGTKEDDFKDV EGKIALIERGDIDFKD
KIANAKKAGAVGVLIYDNQDKGFPIELPNVDQMPAAFI SRRDGLLLKDNP
PKTITFNATPKVLPTASGKLSRFSSWGLTADGNIKPDIAAPGQDILSSV
ANNKYAKLSGTSMSAPLVAGIMGLLQKQYETQYPMTPSERLDLAKKVL
SSATALYDEDEKAYFSPRQGGAGAVDAKKASAATMYVTDKNTSSKVHLN
NVSDKFEVTVTVHNKSDKPQELYYQVTVQTDKVDGKHFALAPKALYETSW
QKITIPANSSKQVTPIDASRFSKDLLAQMKNYFLEGFVRFKQDPTKEE
LMSIPYIGFRGDFGNLSALEKPIYDSKDGSSYYHEANSDAKQDGLDGLQ
FYALKNNFTALTTESNPWTIIKAVKEGVENIEDIESSEITETIFAGTFAK
QDDSHYYIHRHANGKPYAAISPNGDGNRDYVQFGTFLRNAKNLVAEVL
DKEGNVWVTSSEVTEQVVKYNNNDLASTLGSTRFEKTRWDGKDKGKVAN
GTYTYRVRYTPISSGAKEQHTDFDVIDNTTPEVATSATFSTEDSRLTLA
SKPKTSQPVYRERIAITYMDEDLPTTEYISPNEGTFPLPEEAETMEGAT
VPLKMSDFTYVVEDMAGNITYTPVTKLLEGHSNKPEQDGSQAPDKKPEA
KPEQDGSQTPDKKKETKPEKDSGQTPGKTPQKQSSRTLEKRSKRAL
ATKASTRDQLPTTNDKDTNRLHLKLKLVMTTFFLG

GBS 276 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 27 above. In one embodiment, one or more amino acids from the leader or signal sequence region of GBS 276 are removed. An example of such a GBS 276 fragment is set forth below as SEQ ID NO: 28.

SEQ ID NO: 28

QSDIKANTVTEDTPATEQAVEPPQPIAVSEESRSSKETKTSQTPSDVGET
VADDANDLAPQAPAKTADTPATSKATIRDLNDPSHVKTQEKAGKGAGTV
VAVIDAGFDKNHEAWRLTDKTKARYQSKENLEKAKKEHGIYGEWVUDKV
AYYHDYSKDGKNAVDQEHGTHVSGILSGNAPSEMKEPYRLEGAMPEAQLL
LMRVEIVNGLADYARNYAQAIRDAVN LGAKVINMSFGNAALAYANLPDET
KKAFFDYAKSKGVSIVTSAGNDSSFGGKPRPLADHPDYGVVGTAAADST
LTVASYSQKQLTETATVKTDDHQDKEMPVISTNRFEPNKAYDIAYANRG

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TKEDDFKDV EGKIALIERGDIDFKDKIANAKKAGAVGVLIYDNQDKGFPI
ELPNVDQMPAAFI SRRDGLLLKDNPPKTITFUATPKVLPTASGKLSRFS
5 SWGLTADGNIKPDIAAPGQDILSSVANNKYAKLSGTSMSAPLVAGIMGLL
QKQYETQYPMTPSERLDLAKKVLMS SATALYDEDEKAYFSPRQGGAGAV
DAKKASAATMYVTDKNTSSKVHLNUVSDKFEVTVTVHNKSDKPQELYYQ
10 VTVQTDKVDGKHFALAPKALYETSWQKITIPANSSKQVTPIDASRFSKD
LLAQMKNYFLEGFVRFKQDPTKEELMSIPYIGFRGDFGNLSALEKPIYD
SKDGSSYYHEANSDAKQDGLDGLQFYALNNKFTALTTESNPWTIIKAVK
15 EGVENIEDIESSEITETIFAGTFAKQDDSHYYIHRHANGKPYAAISPNG
DGNRDYVQFGTFLRNAKNLVAEVL DKEGNVWVTSSEVTEQVVKYNNNDLA
STLGSTRFEKTRWDGKDKGKVANGTYTYRVRYTPISSGAKEQHTDFDV
20 IVDNTTPEVATSATFSTEDSRLTLASKPKTSQPVYRERIAITYMDEDLPT
TEYISPNEGTFPLPEEAETMEGATVPLKMSDFTYVVEDMAGNITYTPVT
KLLEGHSNKPEQDGSQAPDKKPEAKPEQDGSQTPDKKKETKPEKDSG
25 QTPGKTPQKQSSRTLEKRSKRALATKASTRDQLPTTNDKDTNRLHLKL
LVMTTFFLG

GBS 276 contains a C-terminal transmembrane and/or cytoplasmic region which is indicated by the underlined sequence near the end of SEQ ID NO: 27 above. In one embodiment, one or more amino acids from the transmembrane or cytoplasmic regions of GBS 276 are removed. An example of such a GBS 276 fragment is set forth below as SEQ ID NO: 29.

SEQ ID NO: 29

MRKKQKLPFDKLAIALISTSI LLNAQSDIKANTVTEDTPATEQAVEPPQP
IAVSEESRSSKETKTSQTPSDVGETVADDANDLAPQAPAKTADTPATSKA
40 TIRDLNDPSHVKTQEKAGKGAGTVVAVIDAGFDKNHEAWRLTDKTKARY
QSKENLEKAKKEHGIYGEWVNDKVAYYHDYSKDGKNAVDQEHGTHVSGI
LSGNAPSEMKEPYRLEGAMPEAQLLLMRVEIVNGLADYARNYAQAIRDAV
45 NLGAKVINMSFGNAALAYANLPDETCKAFDYAKSKGVSIVTSAGNDSSF
GKPRPLADHPDYGVVGTAAADSTLTVASYSQKQLTETATVKTDDHQD
KEMPVISTNRFEPNKAYDIAYANRGTKEDDFKDV EGKIALIERGDIDFKD
50 KIANAKKAGAVGVLIYDNQDKGFPIELPNVDQMPAAFI SRRDGLLLKDNP
PKTITFNATPKVLPTASGKLSRFSSWGLTADGNIKPDIAAPGQDILSSV
ANNKYAKLSGTSMSAPLVAGIMGLLQKQYETQYPMTPSERLDLAKKVL
55 SSATALYDEDEKAYFSPRQGGAGAVDAKKASAATMYVTDKNTSSKVHLN
NVSDKFEVTVTVHNKSDKPQELYYQVTVQTDKVDGKHFALAPKALYETSW
QKITIPANSSKQVTPIDASRFSKDLLAQMKNYFLEGFVRFKQDPTKEE
60 LMSIPYIGFRGDFGNLSALEKPIYDSKDGSSYYHEANSDAKQDGLDGLQ
FYALKNNFTALTTESNPWTIIKAVKEGVENIEDIESSEITETIFAGTFAK
QDDSHYYIHRHANGKPYAAISPNGDGNRDYVQFGTFLRNAKNLVAEVL
65 DKEGNVWVTSSEVTEQVVKYNNNDLASTLGSTRFEKTRWDGKDKGKVAN

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GTYYRVRYTPISSGAKEQHTDFDVIDNTTPEVATSATGSTEDSRLTLA
 SKPKTSQPVYRERIAYTYMDEDLPTTEYISPNEDGTFTLPEEAETMEGAT
 VPLKMSDFTYVVEDMAGNITYTPVTKLLEGHNSNKPEQDGSQAPDKKPEA
 KPEQDGSQTPDKKKETKPEKDSSGQTPGKTPQKGQSSRTLEKRSSKRAL
 ATK

In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic regions of GBS 276 are removed. An example of such a GBS 276 fragment is set forth below as SEQ ID NO: 30.

SEQ ID NO: 30
 QSDIKANTVTEDTPATEQAVEPPQPIAVSEESRSSKETKTSQTPSDVGET
 VADDANDLAPQAPAKTADTPATSKATIRDLNDPSHVTKLQEKAGKGAGTV
 VAVIDAGFDKNHEAWRETDKTKARYQS KENLEKAKKEHGI TYGEWVNDKV
 AYYHDYSKDGKNNAVDQEHGTHVSGILSGNAPSEMKEPYRLEGAMPEAQLL
 LMRVEIVNGLADYARNYAQAIRDAVN LGAKVINMSFGNAALAYANLPDET
 KKAFDYAKSKGVSIVTSAGNDSSFGGKPRPLADHPDYGVVGT PAAADST
 LTVASYSPDKQLTETATVKTDHDKEMPVISTNRFEPNKAYDIYANRG
 TKEDDFKDV EKGIALIERGIDIFDKIANAKKAGAVGLIYDNQDKGFPFI
 ELPNVDQMPAAFISRRDGLLLKDNPPKITITFNATPKVLPASGTLKSRFS
 SWGLTADGUIKFDIAAPGQDILSSVANNKYAKLSGTSMSAPLVAGIMGLL
 QKQYETQYPDMTPSERLDLAKKVLMS SATALYDEDEKAYFSPRQQGAGAV
 DAKKASAATMYVTDKNTSSKVHLNNVSDKFEVTVTVHNKSDKPQELYYQ
 VTVQTDKVDGKHFALAPKALYETSWQKITIPANSSKQVTVPIDASRFSKD
 LLAQMKNGYFLEGFVRFKQDPTKEELMSIPYIGFRGDFGNLSALEKPIYD
 SKDGSSYYHEANSDAKQDLGDGLQFYALKNNFTALTTESNPWTIIKAVK
 EGVENIEDIESSEITETIFAGTFAKQDDSHYIHRHANGKPYAAISPNG
 DGNRDYVQFGTFLRNAKNLVAEVL DKEGNVVTSEVTEQVVKNNYNDLA
 STLGSTRFEKTRWDGKDKDGKVVANGTYTYRVRYTPISSGAKEQHTDFDV
 IVDNTTPEVATSATFSTEDSRLTLASKPKTSQPVYRERIAYTYMDEDLPT
 TEYISPNEDGTFTLPEEAETMEGATVPLKMSDFTYVVEDMAGNITYTPVT
 KLEGHNSNKPEQDGSQAPDKKPEAKPEQDGSQTPDKKKETKPEKDSSG
 QTPGKTPQKGQSSRTLEKRSSKRALATK

Further description of GBS 276 can be found in the following references: Qi Chen et al., "Immunization with C5a Peptidase or Peptidase-Type III Polysaccharide conjugate Vaccines Enhances Clearance of Group B Streptococci from Lungs of Infected Mice", *Infection and Immunity* (2002) 70 (11):6409-6415; Beckmann et al., "Identification of Novel Adhesions from Group B Streptococci by Use of Phage Display Reveals that C5a Peptidase Mediates Fibronectin Binding" *Infection and Immunity* (2002) 70(6):2869-2876; Cheng et al., "The Group B Streptococcal C5a Peptidase Is Both a Specific Protease and an Invasin" *Infection and Immunity* (2002) 70(5) 2408-2413; and Cheng et al., "Antibody against Surface-Bound C5a Peptidase Is Opsonic and Initiates Macrophage Killing of Group B Streptococci" *Infection and Immunity* (2001) 69(4):2302-2308.

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GBS 305

GBS 305 refers to a UDP-N-acetylmuramoylalanine—D-glutamate ligase, also referred to as Mur D. Nucleotide and amino acid sequences of GBS 305 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 207 and SEQ ID 208. These sequences are set forth below as SEQ ID NOS 31 and 32:

SEQ ID NO. 31
 ATGGGACGAGTAATGAAAACAATAACAACATTTGAAAATAAAAAAGTTTT
 AGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACGTTTGTAGCTA
 GGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCATTTGATGAAAAT
 CCAACAGCACAGTCTTTGTTGGAAGAGGTATTAAAGTGGTTTGTGGTAG
 TCATCCTTTAGAATTGTTAGATGAGGATTTTGTTCATGATTAAAAATC
 CAGGAATACCTTATAACAATCCTATGGTCAAAAAGCATTAGAAAAACAA
 ATCCCTGTTTTGACTGAAGTGAATTAGCATACTTAGTTTCAGAACTCA
 GCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAACGACAACGATGA
 TTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTTGTAGCTGGGAAT
 ATCGGCTTTCTGCTAGTGAAGTTGTTCCAGGCTGCGAATGATAAAGATAC
 TCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGAGTTAAGGAATTC
 GTCCTCATATTGCAGTAATTACTAATTTAATGCCAACTCATTTAGATTAT
 CATGGGCTCTTTTGAAGATTATGTTGCTGCAAAATGGAATATCCAAATCA
 AATGTCTTCATCTGATTTTGTGGTACTTAATTTAATCAAGGTATTTCTA
 AAGAGTTAGCTAAACTACTAAAGCAACAATCGTTCCTTTCTCTACTACG
 GAAAAGTTGATGGTGCTTACGTACAAGACAAGCAACTTTCTATAAAGG
 GGAGAATATTATGTCAGTAGATGACATTGGTGTCAGGAGCCATAACG
 TAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGGCTGGTATCAGT
 AATCAAGTTATTAGAGAACTTTAAGCAATTTTGGAGGTGTTAAACACCG
 CTTGCAATCACTCGGTAAGGTTTCATGGTATTAGTTTCTATAACGACAGCA
 AGTCAACTAATATATTGGCAACTCAAAAAGCATTATCTGGCTTTGATAAT
 ACTAAAGTTATCCTAATTGCAGGAGGCTTGATCGCGGTAAAGAGTTTGA
 TGAATTGATACCAGATATCACTGGACTTAAACATATGTTGTTTATAGGGG
 AATCGGCATCTCGAGTAAACGTGCTGCACAAAAGCAGGAGTAACCTTAT
 AGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAGCTTATGAGGTGGC
 ACAACAGGGCGATGTTATCTTGCTAAGTCTGCAATGCATCATGGGACA
 TGTATAAGAATTTTGAAGTCCGTGGTGATGAATTCATTGATACTTTTCGAA
 AGTCTTAGAGGAGAG

SEQ ID NO. 32
 MGRVMKTIITFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDEN
 PTAQSLLEEIGKVVCGSHPLELLDEDFCYMIKNGPIYNPNPMVKKALEKQ
 IPVLTVEVELAYLVSESQLIGITGSNGKTTTTTMAIEVLNAGGQRGLLAGN
 IGFPASEVVQAANDKDTLVMELSSFLMGVKEFRPHIAVITNLMPHLDY
 HGSFEDYVAAKWNINQNMSSDFLVNLFNQGISKEAKTTKATIVPFSTT
 EKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGIS
 NQVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDN

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TKVILIAGGLDRGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTY
SDALDVRDAVHKAYEVAQQGDVILLSPANASWDMYKNFEVRGDEFIDTFE
SLRGE

GBS 305 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 32 above. In one embodiment, one or more amino acids from the leader or signal sequence region are removed from GBS 305. An example of such a GBS 305 fragment is set forth below as SEQ ID NO: 33.

SEQ ID NO: 33

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 EEGIKVVCGSHPLELLEDDEFCYMIKNPGIPYNNPMVKKALEKQIPVLTEV
 ELAYLVSESQIGITGSNGKTTTTTMAIEVLNAGGQRGLLAGNIGFPASE
 VVQANNDKDTLVMELSSFQLMGVKEFRPHIAVITNLMPTHLDYHGSFEDY
 VAAKWNIONQMSSDFLVLNFNQGISKEKAKTTKATIVPFSTTEKVDGAY
 VQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
 LSNFPGGVKHLRQSLGKVHGISFYNDKSTNILATQKALSGFDNTKVILIA
 GGLDRGNEFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVR
 DAVHKAYEVAQQGDVILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

GBS 305 contains a C-terminal transmembrane or cytoplasmic region indicated by the underlined sequence near the end of SEQ ID NO: 32 above. In one embodiment, one or more amino acids from the transmembrane or cytoplasmic regions are removed from GBS 305. An example of such a GBS 305 fragment is set forth below as SEQ ID NO: 34.

SEQ ID NO: 34

MGRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDEN
 PTAQSLLLEEGIKVVCGSHPLELLEDDEFCYMIKNPGIPYNNPMVKKALEKQ
 IPVLTEVELAYLVSESQIGITGSNGKTTTTTMAIEVLNAGGQRGLLAGN
 IGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHIAVITNLMPTHLDY
 HGSFEDYVAAKWNIONQMSSDFLVLNFNQGISKEKAKTTKATIVPFSTT
 EKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGIS
 NQVIRETLSNFGGVKHLRQSLGKVHGISFYNDK

In one embodiment one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic regions are removed from GBS 305. An example of such a GBS 305 fragment is set forth below as SEQ ID NO: 35.

SEQ ID NO: 35

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLL
 LLEGIKVVCGSHPLELLEDDEFCYMIKNPGIPYNNPMVKKALEKQIPVL
 EVELAYLVSESQIGITGSNGKTTTTTMAIEVLNAGGQRGLLAGNIGFP
 ASEVVQAANDKDTLVMELSSFQLMGVKEFRPHIAVITNLMPTHLDYHGS
 FEDYVAAKWNIONQMSSDFLVLNFNQGISKEKAKTTKATIVPFSTTEK

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VDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
 QVIRETLSNFGGVKHLRQSLGKVHGISFYNDK

GBS 322

GBS 322 refers to a surface immunogenic protein, also referred to as "sip". Nucleotide and amino acid sequences of GBS 322 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8539 and SEQ ID 8540. These sequences are set forth below as SEQ ID NOS 36 and 37:

SEQ ID NO. 36

ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATC
 AGTCGCAAGTGTTCAAGCACAAGAACAGATACGACGTGGACAGCACGTA
 CTGTTTCAGAGGTAAAGGCTGATTTGGTAAAGCAAGACAATAAATCATCA
 TATACTGTGAAATATGGTGATACACTAAGCGTTATTTCAGAAGCAATGTC
 AATTGATATGAATGCTTAGCAAAAATAAATAACATTGCAGATATCAATC
 TTATTATCCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCAT
 ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAATGCTGCTGGTCA
 AACACAGCTACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGCAGACC
 AAAAGTTTCTCTCAATACAATTCGGAAGGTATGACACCAGAAGCAGCA
 ACAACGATTGTTTCGCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAA
 ATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTA
 ATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCA
 GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAAC
 AACAGTATCACCAGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTA
 AAGTAGCACCGGTAAGAACTGTAGCAGCCCCAGTAGTGCAAGTGTTAA
 GTAGTCACTCCTAAAGTAGAACTGGTGATCACCAGAGCATGTATCAGC
 TCCAGCAGTTCCTGTGACTACGACTTACCAGCTACAGACAGTAAGTTAC
 AAGCGACTGAAGTTAAGAGCGTCCGGTAGCACAAAAGCTCCAACAGCA
 ACACCGGTAGCACAAACAGCTTCAACAACAAATGCAGTAGCTGCACATCC
 TGAATAATGCAGGGCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAG
 CGTCAACTTATGGAGTTAATGAATTCAGTACATACCGTGCAGGAGATCCA
 GGTGATCATGGTAAAGGTTTAGCAGTTGACTTTATTGTAGGTACTAATCA
 AGCACTTGGTAATAAAGTTGCACAGTACTCTACACAAAATATGGCAGCAA
 ATAACATTTTCATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAAC
 AGTATTTATGGACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGG
 CGTTACTGCCAACCACTATGACCAGTTACAGTATCATTAAACAAATAAT
 ATAAAAAGGAAGCTATTTGGCTTCTTTTTATATGCCTTGAATAGACTT
 TCAAGTTCTTATATAATTTTATTA

SEQ ID NO. 37

MNKKVLLTSTMAASLLSVASVQAQETDTTWTARTVSEVKADLVKQDNKSS
 YTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
 TATSMKIETPATNAAGQTTATVDLKTNQSVADQKVSNTISEGMTPEAA
 TTIVSPMKTYSSAPALKSKEVLAQEQAQVQAANEQVSPAPVKISITSEVP

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AAKEEVKPTQTSVSQSTTVSPASVAAETPAVPVAKVAPVRTVAAPRVASVK
 VVTPKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVAQKAPTA
 TPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDP
 GDHGKGLAVDFIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTN
 SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK

GBS 322 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence near the beginning of SEQ ID NO: 37. In one embodiment, one or more amino acids from the leader or signal sequence region of GBS 322 are removed. An example of such a GBS 322 fragment is set forth below as SEQ ID NO: 38.

SEQ ID NO: 38
 DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYFETT
 LTVTYDQKSHATSMKIETPATNAAGQTTATVDLKTNQVSVADQKVS LNT
 ISEGMPPEAATTIVSPMKTYSSAPALKSKEVLAQEQAVSQAAANEQVSPA
 PVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETPAVPVAKVAPVRT
 VAAPRVASVKVVPVKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKS
 VPVAQKAPTATPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVN
 EFSTYRAGDPGDHGKGLAVDFIVGTNQALGNKVAQYSTQNMAANNISYVI
 WQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK

GBS 330

GBS 330 refers to a pyruvate kinase, also referred to as "pyk". Nucleotide and amino acid sequences of GBS 330 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8791 and SEQ ID 8792. These sequences are set forth below as SEQ ID NOS 39 and 40:

SEQ ID NO. 39
 ATGAATAAACGCGTAAAAATCGTTGCAACACTTGGTCCTGCGGTTGAATT
 CCGTGGTGGTAAGAAGTTTGGTGAGTCTGGATACTGGGGTGAAAGCCTTG
 ACGTAGAAGCTTCAGCAGAAAAAATGCTCAATTGATTAAAGAAGGTGCT
 AACGTTTTCGTTTCAACTTCTCACATGGAGATCATGCTGAGCAAGGAGC
 TCGTATGGCTACTGTTTCGTAAGCAGAAGAGATTGCAGGACAAAAAGTTG
 GCTTCCTCCTTGATACTAAAGGACCTGAAATTCGTACAGAACCTTTTGA
 GATGGTGAGATTTCATTATATACAAACAGGTACAAAATTACGTGTTGC
 TACTAAGCAAGGTATCAAACTCAACTCCAGAAGTGATTGCATTGAATGTTG
 CTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGGTAAGCAAACTCCT
 GTTGATGATGGTAACTAGGTCTTACTGTGTTTGCAAAAGATAAAGACAC
 TCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCTTATTGGTAAACAAA
 AAGGTGTAACATCCCTTATACTAAAATTCCTTTCCAGCACTTGACAGAA
 CGCGATAATGCTGATATCCGTTTTGGACTTGAGCAAGGACTTAACTTTAT
 TGCTATCTCATTGTGACGTACTGCTAAAGATGTTAATGAAGTTCGTGCTA
 TTTGTGAAGAACTGGSMATGGACACGTTAAGTTGTTGCTAAAATTGAA
 AATCAACAAGGTATCGATAATATTGATGAGATTATCGAAGCAGCAGATGG

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TATTATGATTGCTCGTGGTGATATGGGTATCGAAGTTCCATTGTAAATGG
 TTCCAGTTTACCAAAAAATGATCATTACTAAAGTTAATGCAGCTGGTAAA
 5 GCAGTTATTACAGCAACAAATATGCTTGAAACAATGACTGATAAACACCG
 TGCGACTCGTTCAGAAGTATCTGATGTCTTCAATGCTGTTATTGATGGTA
 CTGATGCTACAATGCTTTCAGGTGAGTCAGCTAATGGTAAATACCCAGTT
 10 GAGTCAGTTTCGTACAATGGCTACTATTGATAAAAAATGCTCAAACATTACT
 CAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCACGTAATAACAAAA
 CTGATGTTATTGCATCTGCGGTTAAGATGCAACACACTCAATGGATATC
 15 AAAGTTGTTGTAACAATTACTGAAACAGGTAATACAGCTCGTGCCATTTC
 TAAATTCGTCAGATGCAGACATTTTGGCTGTTACATTTGATGAAAAAG
 TACAACGTTTCATTGATGATTAAGTGGGGTGTATCCCTGTCTTGCAGAC
 AAACGAGCATCTACAGATGATATGTTTGAGGTTGCAGAACGTGTAGCACT
 TGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTTATCGTTGCAGGTG
 TTCCTGTAGGTACAGGTGGAACATAACAATCGCTGTTCTGACTGTTAAA

SEQ ID NO. 40
 25 MNKRVKIVATLGPVAFRGGKKFGESEGYWGESLDVEASAEEKIAQLIKEGA
 NVFRFNFSHGDHAEQGMATVRKAEIAGQKVGFLDDTKGPEIRTELFE
 DGADPHSYTTGKLRVATKQGIKSTPEVIALNVAGGLDIFDDVEVGKQIL
 30 VDDGKLGLTVFAKDKDTREFEVVENDGLIGKQKGVNIPYTKIPFALAE
 RDNADIRFLEQGLNFIAISFVRTAKDVNEVRAICEETGXGHVLFKAKIE
 NQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGK
 35 AVITATNMLETMRDKPRTRSEVSDVFNAVIDGTDATMLSGESANGKYPV
 ESVRTMATIDKNAQTLLENYGRDLSSAFPRNNKTDVIASAVKDATHSMDI
 KLVVTITETGNTARAISKFRPDADILAVTFDEKVQRSLMINWGVIPVLAD
 40 KPASTDDMFEVAERVALEAGFVESGDNIIVAGVPVGTGGTNTMRVRTVK

GBS 338

GBS 338 refers to a Sat D protein. Nucleotide and amino acid sequences of GBS 338 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8637 and SEQ ID 8638. These sequences are set forth below as SEQ ID NOS 41 and 42:

SEQ ID NO. 41
 50 TTGTCTGCTATAATAGACAAAAAGGTGGTGATATTTATGTATTAGCATT
 AATCGGTGATATCATTAAATCAAACAGATACTTGAACGTGAACTTTCC
 AACAGTCTTTTCAGCAACTAATGACCGAAGTATCTGATGTATATGGTGAA
 55 GAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCAAGCTTT
 ATTGAAACCATCAAAAAAGGTATTTCAAATTATTGACCATATTCAACTAG
 CTCTAAAACCTGTAAATGTAAGGTTTCGGCTCGGTACAGGAAACATTATA
 ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTGCCTACTG
 GCATGCTCGCTCAGCTATTAATCATATACATGATAAAAAATGATTATGGAA
 CAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACCAAAACCTTGAATTA
 60 AACTAAATAGTCTCATTTAGCTGGTGATTTTATCAAGTCAAAATGGAC
 65 TACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATAATTATC

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AAGAACAATTTCAACATCAAAAGTTAGCCCAACTGGAAAAATTGAACCT
AGTGCCTGACTAAACGCCCTTAAGCAAGCGGTCTGAAGATTTACTTAAAG
AACGAGAACACAGGCAGCCGATCTATTAGTTAAAAGTTGCACTCAAACCTA
AAGGGGAAGCTATGATTTT

SEQ ID NO. 42
MSAIDKKVIFMYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGE
ELISPFTITAGDEFQALLKPSKKVFQIIDHIQLALKPVNVRFLGTGNII
TSINSNESIGADGPAYWHARSAINHIHDKNDYGTVQVAICLDDQNLLE
TLUSLISAGDFIKSKWTTNHFQMLEHLILQDNYQEQQEQLAQLENIEP
SALTKRLKASGLKIYLRTRTQAADLLVKSCQTQKGSYDF

GBS 338 may contain an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 42 above. In one embodiment, one or more amino acids from the leader or signal sequence region are removed from GBS 338. An example of such a GBS 338 fragment is set forth below as SEQ ID NO: 43.

SEQ ID NO: 43
MYLALIGDIINSKQILERETFQQSFQQLMTELSDVYGEELISPFTITAGD
EFQALLKPSKKVFQIIDHIQLALKPVNVRFLGTGNIIITSINSNESIGAD
GPAYWHARSAINHIHDKNDYGTVQVAICLDDQNLLETLNLSLISAGDFI
KSKWTTNHFQMLEHLILQDNYQEQQEQLAQLENIEPSALTKRLKASGL
KIYLRTRTQAADLLVKSCQTQKGSYDF

GBS 361

GBS 361 refers to a cyll protein. Nucleotide and amino acid sequences of GBS 361 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8769 and SEQ ID 8770. These sequences are set forth below as SEQ ID NOS 44 and 45:

SEQ ID NO. 44
ATGAGCGTATATGTTAGTGAATAGGAATTATTTCTTCTTGGGAAAGAA
TTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTA
AACATTTATATAAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGC
ATAACTAGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAA
TTTTAAATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTG
TTAATTTAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTT
GGGGAAAGAGTGCTGGTCAAAATGCCTTGATCAATTTGAAGAAGGAGA
GCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTG
CTGATGAATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATT
TCAACCGCTGTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATT
ACTTCAAGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGT
TAAGTGATATTTCTTTAGCAGGCTTCACATCACTAGGAGCTATTAATACA
GAAATGGCATGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGA
GGGCGCTGGTTTTGTGTTCTGTCAAAGATCAGTCCTTAGCTAAATATG

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GAAAAATTATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCA
CCTAAGCCAACAGGTGAAGGGCGGCACAGATTGCAAGCAGCTAGTGAC
5 TCAAGCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCACGGTA
CAGGTACTCAAGCTAATGATAAAATGAAAAAATATGTATGGTAAGTTT
TTCCCGACACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCATAC
10 TCTAGGGGCTGCAGGTATTATCGAATTGATTAATGTTTACGGCAATAG
AGGAACAGACTGTACCAGCAACTAAAAATGAGATTGGGATAGAAGGTTTT
CCAGAAAAATTTGTCTATCATCAAAAGAGAGAATACCCAATAAGAAATGC
15 TTTAAATTTTTCGTTTGCTTTTGGTGGAATAATAGTGGTGTCTTATTGT
CATCTTTAGATTACCTCTAGAAACATTACCTGCTAGAGAAAAATCTTAA
ATGGCTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTC
TATAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTAC
20 GCTTTAAAGGGGCTAGACCACCCAAAACGTCAACCCAGCACAATTTAGG
AAAATGGATGATTTTCCAAAATGGTTGCCGTAACACAGCTCAAGCACT
AATAGAAAGCAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAA
25 TTGTATTTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGTATTGAA
AAGCAATCACACAGAGGATATGCATGTGTTCTGCTTCACGATTTCC
GTTTACAGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTAAAA
30 TAACAGGTCTTTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGATGGT
ATACAATATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGAT
TCTTGTCTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGAAC
35 AATTAAACTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTTCAGCA
CAAGTCTCTCTCGTCAAGCATTGGATAATTCTCCTATAATATTAGGTAG
TAAACAATTAAATATAGCCATAAAACATTACAGATGTGATGACTATTT
40 TTGATGCTGCGCTTCAAAATTTATTATCAGACTTAGGACTAACCATAAAA
GATATCAAGGTTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAGA
TTATGATTCTTTCAGCGAATTGTCTGAGTATTATAATATGCCAAACCTTG
45 CTTCTGGTCAGTTTGGATTTTCATCTAATGGTGTGGTGAAGAACTGGAC
TATACTGTTAATGAAAGTATAGAAAAGGCTATTATTTAGTCTATCTTA
TTCGATCTTCGGTGGTATCTCTTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 45
MSVYVSGIGIISLKGNYSEHKQHLFDLKEGISKHLKNHDSILESITGS
ITSDPEVPEQYKDETRNFKFAPTAFEEALSSGVNLKAYHNIACVCLGTS
GGKSAGQNALYQFEEGERQVDASLLEKASVYHIADELMAYHDIVGASYVI
55 STACSASNNAVILGTQLLDGDCDLAICGGCDELSDISLAGFTSLGAIN
EMACOPYSSGKGINLGEAGFVVLVKDQSLAKYGKIIGGLITSDGYHITA
PKPTGEGAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGDF
60 PPTTTLISSTKGQTGHTLGAAGIIELINCLAAIEEQVTPATKNEIGIEGF
PENFVYHQKREYPIRNALNGSFAPGGNNSGVLSSSLDSPLETLRARENTLK
MAILSSVASISKNESLSITYEKVASNFNDFEALRFKGPPTKVNPAQFR
65 KMDDFSKMVAVTQAALIESNINLKODTSKVGI VFTTSLGPVEVVEGIE

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KQITTEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTNSGALDG
IQYAKEMMRNDNLDYVILVSNQWTDMSFMWQQLNYDSQMFVGS DYCSA
QVLSRQALDNSPIILGSKQLKYSHKTFTDVTIFDAALQNLLSDLG LTIK
DIKGFVWNERKKAVSSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELD
YTVNESDIEKGYLVLSYSIGGISFAIIEKR

GBS 361 may contain an N-terminal leader or signal
sequence region which is indicated by the underlined
sequence at the beginning of SEQ ID NO: 45 above. In one
embodiment, one or more amino acids from the leader or
signal sequence region are removed from GBS 361. An
example of such a GBS 361 fragment is set forth below as
SEQ ID NO: 46.

SEQ ID NO: 46
VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSD
PEVPEQYKDETRNFKFAFTAFEEALASSGVNLKAYHNI AVLCTSLGGKS
AGQNALYQFEEGERQVDASLLEKASVYHIADELMAYHDIVGASVISTAC
SASNNAVILGTQLLQDGDCLAI CGGCELSDISLAGFTSLGA INTEMAC
OPYSSGKGINLGE GAGFVVLVKDQSLAKYGIIGGLITSDGYHITAPKPT
GEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGDFPPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENF
VYHQKREYPIRNALNGSFAPFGNNSGVLSLSDSPLETLRARENTL KMAIL
SSVASISKNESLSITYEKVASNFNDFEALRFK GARPPKTVNPAQFRKMDD
FSKMVAVTTAQALIESNINLKKODTSKVGIVFTTSLSGPVEVVEGIEKQIT
TEGYAHVSASRFPFTVMNAAAGMLSIIFKITGPLSVISTNSGALDGIQYA
KEMMRNDNLDYVILVSNQWTDMSFMWQQLNYDSQMFVGS DYCSAQVLS
RQALDNSPIILGSKQLKYSHKTFTDVTIFDAALQNLLSDLG LTIKDIKG
FVWNERKKAVSSDYDFLANLSEYNNMPNLASGQFGFSSNGAGEELDYTVN
ESDIEKGYLVLSYSIGGISFAIIEKR

GBS 404

Nucleotide and amino acid sequences of GBS 404
sequenced from serotype V isolated strain 2603 V/R are set
forth in Ref. 2 as SEQ ID 8799 and SEQ ID 8800. These
sequences are set forth below as SEQ ID NOS 47 and 48:

SEQ ID NO. 47
ATGAAAATAGATGACCTAAGAAAAGCGACAATGTTGAAGATCGTCGCTC
CAGTAGCGGAGGTTCTTCTCTAGCGGAGGAAGTGATTACCGATTCTTC
AACTTTTATTGCTGCGAGGGAGTTGGAAAACCAAGCTTGTGGTTTTAATC
ATCTTACTGCTACTTGGCGGAGGGGACTAACCAGCATTTTTTAATGACTC
ATCCTCACCTTCTAGTTACCAATCTCAGAAATGTCTCAGTCTCTGTTGATA
ATAGCGCAACGAGAGAACAAATCGATTTCTGTTAATAAAGTCCTTGGCTCA
ACTGAGGATTTCTGGTCACAAGAATTCCAAACCCAAGGTTTGGAAATTA
TAAGGAACCAAACTTGTGTTTACCAATTCAATTCAAACAGGTTGTG
GTATAGGTGAATCTGCTTCAGGACCATTTTATTGTT CAGCAGATAAAAAA
ATCTATCTTGATATTTCTTTTACAATGAATTATCACATAAATATGTGTC

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TACTGGTGATTTTGCTATGGCCTACGTCATCGCCACGAAAGTTGGTCACC
ACATTCAAACAGAGTTAGGCATTATGGATAAGTATAATAGAATGCGACAC
GGACTTACTAAGAAAGAACAAATGCTTTAAATGTTCCGCTAGAACTTCA
AGCAGATTATTATGCAGGGGTATGGGCTCACTACATCAGGGGAAAAAATC
TCTTAGAACAAAGGAGACTTTGAAGAGGCCATGAATGCTGCCACGCCGCTC
GGAGACGATACCCCTTCAGAAAGAAACCTACGGAAAATTAGTGCTGTATAG
CTTTACCCATGGAACAGCTGAACAACGCCAAGTTGGTTTAAACAAAGGCT
TTCAATATGGTGACATCCAACACGGTGATACTTTCTCCGTAGAACATCTA
MKIDDLRKSDNVEDRRSSSGGSFSSGSGSLPILQLLLLRGSKWTKLVVLI
ILLLGGGGLTSIFNDSSSPSSYSQSNVSRVSDNSATREQIDFVNKVLGS
TEDFWSQEFQTQGFNGYKEPKLVLYTNSIQTGCGIGESASGPFYCSADKK
IYLDISFYNELSHKYGATGDFAMAYVIAHEVGHHIQTELGIMDKYNMRH
GLTKKEANALNVRLELQADYYAGVWAHYIRGNLLEQDGFEEAMNAHAV
GDDTLQKETYGKLVDPDSFTHGTAEQRQRWFNKGFGYQYDGIQHGDTFSEHL

GBS 690

Nucleotide and amino acid sequences of GBS 690
sequenced from serotype V isolated strain 2603 V/R are set
forth in Ref. 2 as SEQ ID 9965 and SEQ ID 9966. These
sequences are set forth as SEQ ID NOS 49 and 50 below:

SEQ ID NO. 49
ATGAGTAAACGACAAAAATTTAGGAATTAGTAAAAAGGAGCAATTATATC
AGGGCTCTCAGTGGCCTAATTTAGTAGTAATAGTGGCTTTTATGGGTAC
AATCTCAACCTAATAAGAGTGCAGTAAAACTAACTACAAAGTTTTTAAAT
GTTAGAGAAGGAAGTGTTTCGTCCTCAACTCTTTTACAGGAAAAGCTAA
GGCTAATCAAGAACAGTATGTGTATTTTATGCTAATAAAGGTAATCGAG
CAACTGTACAGTTAAAGTGGGTGATAAAATCACAGCTGGTCAGCAGTTA
GTTCAATATGATACAACAACCTGCACAAGCAGCTACGACACTGCTAATCG
TCAATTAAATAAAGTAGCGCGTCAGATTAATAATCTAAAGACAACAGGAA
GTCTTCAGCTATGGAATCAAGTGATCAATCTTCTTCATCATCACAAAGGA
CAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTCTACAGCAAAATTA
TCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTCAAGATTTGAATG
ATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAGCACAAAAGCATTG
AATGATACTGTTATTACAAGTGACGTATCAGGGACAGTTGTTGAAGTTAA
TAGTGATATTGATCCAGCTTCAAAAACCTAGTCAAGTACTTGTCCATGTAG
CAACTGAAGGTAACTCCAAGTACAAGAACGATGAGTGAGTATGATTTG
GCTAATGTTAAAAAAGACCAGGCTGTTAAAAATAAATCTAAGGTCTATCC
TGACAAGGAATGGGAAGGTAAAAATTCATATATCTCAAATTATCCAGAAG
CAGAAGCAACAACAATGACTCTAATAACGGCTCTAGTGCTGTAATTTAT
AAATATAAAGTAGATATTACTAGCCCTCTCGATGCATTAACAAAGGTTT
TACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCACCTTATTGTCCCTA
CAAGTTCTGTGATAACAAAGATAATAAACACTTTGTTGGGTATACAAAT

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GATTCTAATCGTAAATTTCCAAAGTTGAAGTCAAATTTGGTAAAGCTGA
TGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCAGGACAAATCGTGG
TTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAAATTGATAATATT
GAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGGTGAAA

SEQ ID NO. 50
MSKRQNLGISKKGAIISGLSVALIVVIGGFLWVQSQPNKSAVKNTYKVFN
VREGSVSSSTLLTGKAKANQEYVYFPDANKGNRATVTVKVGDKITAGQQL
VQYDTTTAQAAAYDTANRQLNKVARQINNLTGSLPAMESSDQSSSSSQG
QGTQSTSGATNRLQONQYQSQANASYNQQLDLNDAYADAQAEVNKAQKAL
NDTVITSDVSGTVVEVNSDIDPASKTSQVLVHVATEGKLQVQGTMSYDL
ANVKDQAVKIKSKVYPDKKEWEGKISYISNYPEAEANNNDNNSSAVNY
KYKVDITSPDLALKQGGFTVSEVNVNGDKHLIVPTSSVINKDNKHFVWVYN
DSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNI
ESIDLNSNKKSEVK

GBS 690 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 50 above. In one embodiment, one or more amino acids from the leader or signal sequence region of GBS 690 are removed. An example of such a GBS 690 fragment is set forth below as SEQ ID NO: 51.

SEQ ID NO: 51
FLWVQSQPNKSAVKNTYKVFNVREGSVSSSTLLTGKAKANQEYVYFDAN
KGNRATVTVKVGDKITAGQQLVQYDTTTAQAAAYDTANRQLNKVARQINNLT
KTTGSLPAMESSDQSSSSSQGGTQSTSGATNRLQONQYQSQANASYNQQL
QDLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQV
LVHVATEGKLQVQGTMSYDLANVKDQAVKIKSKVYPDKKEWEGKISYIS
NYPEAEANNNDNNSSAVNYKYKVDITSPDLALKQGGFTVSEVNVNGDKH
LIVPTSSVINKDNKHFVWVYNDNRKISKVEVKIGKADAKTQEILSGLKA
GQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

GBS 691

GBS 691 refers to an iron compound ABC transporter, or a substrate binding protein. Nucleotide and amino acid sequences of GBS 691 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 3691 and SEQ ID 3692. These sequences are set forth as SEQ ID NOS 52 and 53 below:

SEQ ID NO. 52
ATGAAAAAATTGGAATTATTGTCTCAGTACTGACCTTCTTTTGGT
ATCTTGCGGACAACAACTAAACAAGAAAGCACTAAAACACTATTCTA
AAATGCCTAAATTAAGGCTTACCTATTATGAAAAATTCCTGAAAA
CCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTATTTATTA
ACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCC
CCGTTTTTGGTAAACAACTGAAAGAAGCTAAAAAATAACTGCTGATGAT
ACAGAAGCTATTGCCGCACAAAAACCTGATTAAATCATGGTTTTTCGATCA

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AGATCCAAACATCAATACTCTGAAAAAATTGCACCAACTTTAGTTATTA
AATATGGTGCACAAAATTATTTAGATATGATGCCAGCCTTGGGGAAAGTA
5 TTCGGTAAAGAAAAAGAAGCTAATCAGTGGGTAGCCAATGGAAAACTAA
AACTCTCGCTGTCAAAAAAGATTACACCATATCTTAAAGCCTAACACTA
CTTTTACTATTATGGATTTTTATGATAAAATATCTATTATATGTTAAT
10 AATTTTGGACGCGGTGGAGAACTAATCTATGATTCAGTGGTTATGCTGC
CCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTACCGTTT
CGCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTTGTTAATATA
15 AACAAACGACTAAAAAGCAGCTTCATCACTTAAAGAAAGTATGCTCTG
GAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAACTACG
ACGTGTTTTATTCTCTGACCCTCTATCTTTAGAAGCTCAATTAATCA
20 TTTACAAAGGCTATCAAGAAAAATACAAAT

SEQ ID NO. 53
MKKIGIIVLTLLTFFLVSCGQQTQESTKTTISKMPKIEGFTTYGKIPEN
PKKVINFYTSYTGILLKLGVNVSYSLDLEKDSVPVFGKQLEAKKLTTADD
25 TEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMMPALGKV
FGKEKEANQWVSQWKTTLAVKKDLHHILKPNNTFTIMDFYDKNIYLYGN
NFRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIGDYVDYALVNI
30 NKTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVYFSPLSLEAQLKSF
TKAIKENTN

GBS 691 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 53 above. In one embodiment, one or more amino acids are removed from the leader or signal sequence region of GBS 691. An example of such a GBS 691 fragment is set forth below as SEQ ID NO: 54.

SEQ ID NO: 54
EGFTTYGKIPENPKKVINFYTSYTGILLKLGVNVSYSLDLEKDSVPVFGK
QLEAKKLTTADDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQ
45 NYLDMMPALGKVFGEKEANQWVSQWKTTLAVKKDLHHILKPNNTFTIM
DFYDKUIYLYGNFRGGELIYDSLGYAAPEKVKKDVFKKGWFTVSQEAIG
GDYVDYALVNIKNTTKKAASSLKESDVWKNLPAVKKGHIIESNYDVYF
50 SDPLSLEAQLKSFTKAIKENTN

GBS 691 contains a C-terminal transmembrane or cytoplasmic region which is indicated by the underlined sequence at the end of SEQ ID NO: 53 above. In one embodiment, one or more amino acids are removed from the transmembrane or cytoplasmic region of GBS 691. An example of such a GBS 691 fragment is set forth below as SEQ ID NO: 55.

SEQ ID NO: 55
MKKIGIIVLTLLTFFLVSCGQQTQESTKTTISKMPKIEGFTTYGKIPEN
PKKVINFYTSYTGILLKLGVNVSYSLDLEKDSVPVFGKQLEAKKLTTADD
TEAIAAQKPDLMVFDQDPNINTLKKIAPTLLVIKYGAQNYLDMMPALGKV
65 FGKEKEANQWVSQWKTTLAVKKDLHHILKPNNTFTIMDFYDKNIYLYGN

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NFGRGGELIYDSLGYAAPEKVKVDVFKKGWFTVSQEAIGDYVGDYALVNI
 NKTTKKAASSLKESDVWKNLPAVKKGHIIIESNYDVFFYSPLSLEAQLK
 SFT

In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic region are removed from GBS 691. One example of such a GBS 691 fragment is set forth below as SEQ ID NO: 56

SEQ ID NO: 56
 EGFTYYGKIPENPKKVINFTYSYTGILLKLVNVSSYSLDLEKDSPVFGK
 QLKEAKKLTADDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQ
 NYLDMMPALGKVFGEKEANQWVSQWKTKTLAVKKDLHHILKPNNTFTIM
 DFDYDKUIYLYGNFGRGGELIYDSLGYAAPEKVKVDVFKKGWFTVSQEA
 GDIYVGDYALVNIKNTTAKAASSLKESDVWKNLPAVKKGHIIIESNYDVFF
 SDPLSLEAQLKSFT

Additional examples of GBS antigens which may be used in combination with GBS 80 are set forth below.
 GBS 4

GBS 4 refers to another putative cell wall surface anchor family protein. Nucleotide and amino acid sequences of GBS 4 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 1 and SEQ ID 2. These sequences are also set forth below as SEQ ID NOS 57 and 58:

SEQ ID NO. 57
 ATGAAAGTAAAAATAAGATTTTAAACGATGGTAGCACTTACTGTCTTAAC
 ATGTGCTACTTATTATCATCAATCGGTTATGCTGATACAAGTGATAAGAATA
 CTGACACGAGTGTCTGACTACGACCTTATCTGAGGAGAAAAGATCAGAT
 GAACTAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTC
 ATCAAGTGAACAGAAACAAATCCGTCACATAATCCACCTACAACAGAAC
 CATCGCAACCTCACCTAGTGAAGAGAACAGCCTGATGGTAGAACGAAG
 ACAGAAATTGGCAATAATAAGGATATTTCTAGTGAACAAAAGTATTAAT
 TTCAGAAGATAGTATTAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAG
 AAGTGGATCGCGATGAATCATCATCTTCAAAGCAAATGATGGGAAAAAA
 GGCCACAGTAAGCCTAAAAAGGAACCTCCTAAAAACAGGAGATAGCCACTC
 AGATACTGTAATAGCATCTACGGGAGGATTATTCTGTTATCATTAGTT
 TTACAATAAGAAAATGAACTTTAT

SEQ ID NO. 58
 MKVKNKILTMVALTTLTCAATYSSIGYADTSDKNTDTSVVTTLSEEKRS
 ELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQSPSEENKPDGRK
 TEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSKANDGKK
 GHSPKPKELPKTGDSHSDTVIASTGGIILLSLSFYNKKMKLY

GBS 4 contains an N-terminal leader or signal sequence which is underlined at the beginning of SEQ ID NO: 58 above. In one embodiment, one or more amino acids from the N-terminal leader or signal peptide domain of GBS 4 are removed. An example of such a GBS 4 fragment is set forth below as SEQ ID NO 59.

SEQ ID NO 59

DTSDKNTDTSVVTTLSEEKRSDELQSSSTGSSSENESSSSSEPETNPST

5 NPPTTEPSQSPSEENKPDGRKTEIGNNKDISSGTVLISEDSIKNFSK

ASSDQEEVDRDESSSKANDGKKGHSPKPKELPKTGDSHSDTVIASTGGI

10 ILLSLSFYNKKMKLY

A further N-terminal section of GBS 4 may be removed to facilitate recombinant expression. An example of such a GBS 4 fragment is set forth below as SEQ ID NO: 60.

15 SEQ ID NO: 60
 DQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQSPSEENKPDGRKTE
 IGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSKANDGKKGH
 20 SKPKKELPKTGDSHSDTVIASTGGIILLSLSFYNKKMKLY

GBS 4 contains an C-terminal transmembrane region which is underlined at the end of SEQ ID NO: 58 above. In one embodiment, one or more amino acids from the C-terminal transmembrane region is removed. An example of such a GBS 4 fragment is set forth below as SEQ ID NO: 61.

30 SEQ ID NO: 61
 MKVKNKILTMVALTTLTCAATYSSIGYADTSDKNTDTSVVTTLSEEKRS
 ELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQSPSEENKPDGRK
 TEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSKANDGKK
 35 GHSPKPKKE

In one embodiment, both the N-terminal leader or signal domain and the C-terminal transmembrane domain are removed from the GBS 4 sequence. An example of such a GBS 4 fragment is set forth below as SEQ ID NO: 62.

40 SEQ ID NO: 62
 DTSDKNTDTSVVTTLSEEKRSDELQSSSTGSSSENESSSSSEPETNPST
 45 NPPTTEPSQSPSEENKPDGRKTEIGNNKDISSGTVLISEDSIKNGSD
 ASSDQEEVDRDESSSKANDGKKGHSPKPKKE

In yet another embodiment, the N-terminal leader or signal domain, a further N-terminal region and the C-terminal transmembrane domain are removed from the GBS 4 sequence. An example of such a GBS 4 fragment is set forth below as SEQ ID NO: 63.

50 SEQ ID NO: 63
 DQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQSPSEENKPDGRKTE
 IGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSKANDGKKGH
 55 SKPKKKE

GBS 22

GBS 22 refers to a putative adhesion lipoprotein. Nucleotide and amino acid sequences of GBS 22 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ 8583 and SEQ ID 8584. These sequences are set forth below as SEQ ID NOS 64 and 65:

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SEQ ID NO. 64
 ATGAAAAGGATACGGAAGCCTTATTTTGTCTCGAGTAGTTACCTT
 AATTGCTTATGTGCTTGTACTAAACAAAGCCAGCAAAAAATGGCTTGT
 CAGTACTGACTAGCTTTTATCCAGTATATTCCATTACAAAAGCAGTTTCT
 GGTGATTGAATGATATTAATAATGATTGATCAGTCACAGTCAGGTATTATGCG
 TTTTGAACCTCATCAAGTATGTTGCTGCCATTTATGATGCTGATCTAT
 TTCTTTATCATTGCGACACTAGAACCTTGGGCGAGACGTTTGAACCT
 AGTTGTCATCACTCTAAAGTATCTGTAATTGAAGCTTCAAAAGGTATGAC
 TTTGGATAAAGTTCATGGCTTAGAAGATGTAGAGGCAGAAAAAGGAGTAG
 ATGAGTCAACCTTGATGACCTCACACTTGAATGACCTGTAAAAGTA
 TCTGAGGAAGCACAACCTCATCGCTACACAATTAGCTAAAAAGGATCCTAA
 AAACGCTAAGGTTTATCAAAAAATGCTGATCAATTTAGTGACAAGGCAA
 TGGCTATTGCAGAGAAGTATAAGCCAAAATTTAAGCTGCAAGTCTAAA
 TACTTTGTGACTTACATACAGCATTCTCATACTTAGCTAAGCGATACGG
 ATTGACTCAGTTAGGTATTGCAGGTGTCTCACCAGCAAGAACCTAGTGC
 TAAAAAATTAGCCGAATTCAGGAGTTTGTGAAAACATATAAGGTTAAGA
 CTATTTTGTGTAAGAAGGAGTCTCACCTAAATTAGCTCAAGCAGTAGCT
 TCAGCTACTCGAGTTAAAATTGCAAGTTTAAAGTCCCTTARAAGCAGTTCC
 CAAAAACAATAAAGATTACTTAGAAAAATTTGGAACCTAATCTTAAGGTAC
 TTGTCAAATCGTTAAATCAATAG

SEQ ID NO. 65
 MKRIRKSLIFVLGVVTLICLCACTKQSQKNGLSVVTSTFPVYSITKAVS
 GDLNDIKMIRSQSGIHGFEPSSSDVAAYDADFLYSHSTLEAWARRLEP
 SLHHSKVSVEIASKGMTLDKVHGLEDEAEKGVDESTLYDPHTWNPVKV
 SEEAQLIATQLAKKDPKNAKVYQKNADQFSDKAMAI AEKYKPKFAAKSK
 YFVTSHTAFSYLAKRYGLTQLGIAGVSTEQEPSAKKLAIEQEFVKTYKVK
 TIGVEEVGSPKLAQAVASATRVKIASLSPLXAVPKNNKDYLENLETNLKV
 LVKSLNQ

GBS 85

GBS 85 refers to a putative cell division protein (DivIB). Nucleotide and amino acid sequences of GBS 85 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 215 and SEQ ID 216. These sequences are set forth below as SEQ ID NOS 66 and 67:

SEQ ID NO. 66
 ATGCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGTTGTCTTAAC
 GGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGCAAGAAGATG
 AAGAAGAACAAAAACGTATTAAACGAAAAATTACGCTTAGATAAAAGAAGT
 AAATTAAATATTTCTTCTCTGAAGAACCTCAAATACTACTAAAATTAA
 GAAGCTTCATTTTCCAAGATTTCAAGACCTAAGATTGAAAAGAAACAGA
 AAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCATTAGAACT
 GCACCTATATTTGTAGTAGCATTCTAGTCATTTTAGTTTCCGTTTTCCT
 ACTAATCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGGAATCAGC

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ATACACCTGATGATATTTTGTAGAGAAAACGAATATTCAAAAAACGAT
 TATTTCTTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGTTTAGC
 5 TGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATTTCCCA
 ATAAGTTTCATATTCAAGTTCAAGAAAAATAAGATTATTGCATATGCACAT
 ACAAGCAAGGATATCAACCTGTCTTGAAACTGAAAAAAGGCTGATCC
 10 TGTAATAGTTTCAAGCTACCAAAGCACTTCTTAACAATTAACCTTGATA
 AGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCTTTAGACCTT
 GATTTAATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATTCTAAAACGAC
 15 ACCTGACCTCCTGCTGTTAGATATGCACGATGGAAATAGTATTAGAATAC
 CATTATCTAAATTTAAAGAAAGACTTCTTTTACAAACAAATTAAGAAG
 AACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAAC
 AACAAATACCATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAAATA
 20 AATCAACTGATAAAACACAAACACAAATGGTCAGGTTGCGGAAAAATAGT
 CAAGGACAAACAAATAACTCAAATACTAATCAACAAGGACACAGATAGC
 AACAGAGCAGGCACCTAACCTTCAAAATGTTAAT

SEQ ID NO. 67
 MPKKKSDTPEKEEVLTWQKRNLEFLKKRKEDEEQKRINEKLRLDKRS
 KLNISPEEPQNTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNIRIT
 30 APIFVVAFLVILVSVFLLPFSKQKITVSGNQHTPDDILIEKTNIQKND
 YFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQFPNKFHIQVQENKI IAYAH
 TKQGYQPVLETGKKADPVNSSELPKHFLTINLKDSEIKLLIKDLKALDP
 35 DLISEIQVISLADSKTTPDLLLDMHDGNSIRIPLSKFKERLPFYQIKK
 NLKEPSIVDMVEGVYTTNTIESTPDKAEDTKNKSTDKTQTQNGQVAENS
 QGQTNNSTNTNQGGQQIATEQAPNPQNVN

GBS 147

GBS 147 refers to a putative protease. Nucleotide and amino acid sequences of GBS 147 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8525 and SEQ ID 8526. These sequences are set forth below as SEQ ID NOS 68 and 69.

SEQ ID NO. 68
 GTGGATAAACATCACTCAAAAAAGGCTATTTTAAAGTTAACCTTATAAC
 50 AACTAGTATTTTATTAATGCATAGCAATCAAGTGAATGCAGAGGAGCAAG
 AATTAAAAACCAAGAGCAATCACCTGTAATTGCTAATGTTGCTCAACAG
 CCATCGCCATCGGTAACTACTAATACTGTTGAAAAACATCTGTAACAGC
 55 TGCTTCTGCTAGTAATACAGCGAAAGAAATGGGTGATACATCTGTAACAA
 ATGACAAAAACAGAAGATGAATTATTAGAAGAGTTATCTAAAACTTGAT
 ACGTCTAATTTGGGGGCTGATCTTGAAGAAGATATCCCTCTAAACCAGA
 60 GACAACCAACAATAAAGAAAGCAATGTAGTAACAAATGCTTCAACTGCAA
 TAGCACAGAAAGTTCCCTCAGCATATGAAGAGGTGAAGCAGAAAGCAAG
 TCATCGCTTGCTGTTCTTGATACATCTAAAAATAACAAATTAACAAGCCAT
 AACCCAAAGAGGAAAGGAAATGTAGTAGCTATTATTGATACTGGCTTTG
 65 ATATTAACCATGATATTTTTCGTTTAGATAGCCCAAGATGATAAGCAC

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AGCTTTAAACTAAGACAGAATTTGAGGAATTAAGCAAAACATAATAT
 CACTTATGGGAAATGGGTTAACGATAAGATTGTTTTGACATAAATACG
 CCAACAATACAGAAACGGTGGCTGATATTGCAGCAGCTATGAAAGATGGT
 TATGGTTCAGAAGCAAAGAATATTTGCGATGGTACACACGTTGCTGGTAT
 TTTTGTAGGTAATAGTAAACGTCAGCAATCAATGGTCTTCTTTTAGAAG
 GTGCAGCGCCAAATGCTCAAGTCTTATTAATGCGTATTCCAGATAAAAT
 GATTTCGACAAAATTTGGTGAAGCATATGCTAAAGCAATCACAGACGCTGT
 TAATCTAGGAGCAAAACGATTAAATATGAGTATTGGAAAAACAGCTGATT
 CTTTAATTGCTCTCAATGATAAAGTTAAATTAGCACTTAATTAGCTTCT
 GAGAAGGGCGTTGCGATTGTTGTGGCTGCCGAAATGAAGGCGCATTTGG
 TATGGATTATAGCAAACCATTTCAACTAATCCTGACTACGGTACGGTTA
 ATAGTCCAGCTATTTCTGAAGATACTTTGAGTGTGCTAGCTATGAATCA
 CTTAAACTATCAGTGAGGTCGTTGAAACAACTATTGAAGGTAAGTTAGT
 TAAGTTGCCGATTGTGACTTCTAAACCTTTTGACAAAGGTAAGGCCTACG
 ATGTGGTTTATGCCAATTATGGTGCAAAAAAGACTTTGAAGGTAAGGAC
 TTTAAAGGTAAGATTGCATTAATTGAGCGTGGTGGACTTGATTTTAT
 GACTAAAATCACTCATGCTACAAATGCAGGTGTTGTTGGTATCGTTATTT
 TTAACGATCAAGAAAAACGTGAAATTTTCTAATTCCTTACCGTGAATTA
 CCTGTGGGATTATTAGTAAAGTAGATGGCGAGCGTATAAAAAATACTTC
 AAGTCAGTTAACATTTAACCAGAGTTTGAAGTAGTTGATAGCCAAGGTG
 GTAATCGTATGCTGGAACAATCAAGTTGGGCGTGACAGCTGAAGGAGCA
 ATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAATTTATTCTTCAACCTA
 TAATAATCAATACCAACAATGTCTGGTACAAGTATGGCTTCACCACATG
 TTGCAGGATTAATGACAATGCTTCAAAGTCATTTGGCTGAGAAATATAAA
 GGGATGAATTTAGATTCTAAAAAATTGCTAGAATTGCTAAAAACATCCT
 CATGAGCTCAGCAACAGCATTATATAGTGAAGAGGATAAGGCGTTTTATT
 CACCACGTGACGAAGGTGACAGGTGATTTGATGCTGAAAAAGCTATCCAA
 GCTCAATATTATATTACTGGAACGATGGCAAGCTAAAAATTAATCTCAA
 ACGAATGGGAGATAAATTTGATATCACAGTTACAATTCATAAACTTGTA
 AAGGTGTCAAGAATTGTATTATCAAGCTAATGTAGCAACAGAACAGTA
 AATAAAGGTAAATTTGCCCTTAAACCACAAGCCTGCTAGATACTAATTG
 GCAGAAAGTAATCTTCGTGATAAAGAAACACAAGTTCGATTACTATTG
 ATGCTAGTCAATTTAGTCAGAAATTAAGAAGCAGATGGCAATGGTTAT
 TTCTTAGAAGGTTTTGTACGTTTTAAAGAAGCCAGGATAGTAATCAGGA
 GTTAATGAGTATTCCTTTTGTAGGATTTAATGGTGATTTTGCGAACCTAC
 AAGCACTTGAACACCGATTATTAAGACGCTTTCTAAGGTAGTTTCTAC
 TATAAACCAATGATACAACTCATAAAGACCAATTGGAGTACAATGAATC
 AGCTCCTTTTGAAGCAACAACATACTGCCTTGTTAACACAATCAGCGT
 CTTGGGGCTATGTTGATTATGTCAAAATGGTGGGAGTTAGAATTAGCA
 CCGGAGAGTCCAAAAAGAATTATTTTAGGAACTTTGAAGAATAAGGTTGA

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GGATAAAACAATTCATCTTTTGGAAAGAGATGCAGCGAATAATCCATATT
 TTGCCATTTCTCCAAATAAAGATGGAAATAGGGACGAAATCACTCCCCAG
 5 GCAACTTTCTTAAGAAATGTTAAGGATATTTCTGCTCAAGTTCTAGATCA
 AAATGGAAATGTTATTTGGCAAAGTAAGGTTTTACCATCTTATCGTAAAA
 ATTTCCATAATAATCCAAAGCAAAGTGATGGTCATTATCGTATGGATGCT
 10 CTTCACTGAGTGGTGGTTAGATAAGGATGGCAAAAGTTGTGCAGATGGTTT
 TTATACTTATCGCTTACGTTACACACCCAGTAGCAGAAGGAGCAAAATAGTC
 AGGAGTCAGACTTTAAAGTACAAGTAAGTACTAAGTCACCAAATCTTCTCT
 15 TCACGAGCTCAGTTTGTGATGAACTAATCGAACATTAAAGCTTAGCCATGCC
 TAAGGAAAGTAGTTATGTTCTACATATCGTTTACAATTAGTTTTATCTC
 ATGTTGTAAAAGATGAAGAATATGGGGATGAGACTTCTTACCATTATTTCT
 CATATAGATCAAGAAGGTAAAGTGACACTTCTTAAACGGTAAAGATAGG
 20 AGAGAGTGAGGTTGCGGTAGACCCCTAAGGCCTTGACACTTGTGTGGAAG
 ATAAAGCTGGTAATTTTCGCAACGGTAAAATGTCTGATCTCTTGAATAAG
 GCAGTAGTATCAGAGAAAGAAAACGCTATAGTAATTTCTAACAGTTTCAA
 25 ATATTTTGATAACTTGAAAAAAGAACCTATGTTTATTTCTAAAAAAGAAA
 AAGTAGTAAACAAGATCTAGAAGAAATAATATTAGTTAAGCCGCAAACT
 ACAGTTACTACTCAATCATTTGTCTAAAGAAATAACTAAATCAGGAAATGA
 30 GAAAGTCCTCACTTCTACAAACAATAATAGTAGCAGAGTAGCTAAGATCA
 TATCACCTAAACATAACGGGGATTCTGTTAACCATACCTTACCTAGTACA
 TCAGATAGAGCAACGAATGGTCTATTTGTTGGTACTTTGGCATTGTTATC
 35 TAGTTTACTTCTTTATTTGAAACCCAAAAAGACTAAAAATAATAGTAAA
 SEQ ID NO. 69
VDKHHSSKKAILKLTLITTSILLMHSNQVNAEEQELKNQEQSPVIANVAQQ
 40 PPSVTTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDELLEELSKNLD
 TSNLGADLEEYPSKPEPTNNKESVNNNTASTAIAQKVP SAYEEV KPESK
 SSLAVLDTSKITKLQAITQRGKGNVVAI IDTGFDINHDI FRLDSPKDDKH
 SFKTKTEFEELKAKHNI TYGKWVNDKIVFAHN YANNNTETVADIAAMKDG
 45 YGDEAKNISGHVHAGI FVGN SKRPAINGLLLEGAAPNAQVLLMRIPDKI
 DSDKFGEAYAKAI TDAVNLGAKTINMSIGKTADSLIALNDKVKLALKLAS
 EKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISEDLSVASYES
 50 LKTI SEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
 FKGKIALIERGGGLDFMTKI THATNAGVVGVIGNDQEKRGNFILIPYREL
 PVGIISKVDGERIKNTSSQLTFNQSFVVDSSQGGNRMLQSSWGVTAEGA
 55 IKPDVTASGFEIYSSTYNNQYQTMSTGSMASPHVAGLMTMLQSHLAEKYK
 GMNLDSKKLLELSKNILMSSATALYSEEDKAFYSRQQGAGVVD AEKAIQ
 AQYYITGNDGKAKINLKRMDKFDITVTIHKLVEGVKELYQANVATEQV
 60 NKGK FALKPQALLD TNWQKVI LRDKETQVRFTIDASQFSQKLKEQMANGY
 GLEGFVRGKEAKDSNQELMSIPFVGFGNGDFANLQALETPIYKTL SKGSFY
 YKPNDTTHKDQLEYNESAPFESNNY TALLTQSASWGYVDYVKNNGELELA
 65 PESPKRIILGTFENKVEDKTIHLERDAANNPYFAISPNDG NRDEITPQ

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ATFLRNVKDISAQVLDQNGNVIWQSKVLPSYRKNFHNPNKQSDGHYRMDA
 LQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDGKVVSTKSPNLP
 SRAQFDETNRTLSLAMPKESYVPTYLQVLVSHVVKDEEYGDETSYHYFH
 IDQEGKVTLPKTTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNK
 AVVSEKANAIVISNSPKYFDNLKKEPMFISKKEKVVNKNLEEIIILVKPQT
 TVTTQSLSKKEITKSGNEKVLSTNNSSRVAKIISPKNHGDVSNHTLPST
SDRATNGLFVGTLLALLSSLLLYLKPKKTKNNSK

GBS 147 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO 69 above. In one embodiment, one or more amino acids from the leader or signal sequence region of GBS 147 are removed. An example of such a GBS 147 fragment is set forth below as SEQ ID NO: 70.

SEQ ID NO: 70

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASANTAKEMGDT
 SVKNDKTEDELLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVINA
 STAIQKVPASAYEEVKPESKSSLAVLDTSKITKLQAITQRGKGNVVAIID
 TGF DINHDI FRLDSPKDDKHSFKTKTEFEELKAKHNITYGKWVNDKIVFA
 HNYANNNTETVADIAAMKDGDEAKNISHGTHVAGIFVGN SKRPAINGL
 LLEGAAPNAQVLLMRIPDKIDSDFGEAYAKAITDAVNLGAKTINMSGK
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDY
 GTVNSPAISEDLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKG
 KAYDVVYANYGAKDFEGKDFKGKIALIERGGGLDFMTKI THATNAGVVG
 IVIGNDQERKGNFLIPYREL PVGIIISKVDGERIKNTSSQLTFNQSFVVD
 SQGGNRMLEQSSWGVTAEAGAIKPDVTASGFEIYSSYNNQYQTMSTGMA
 SPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNI LMSSATALYSEEDK
 AFYSRQGGAGVDAEKAIQAQYYITGNDGKAKINLKRMDKFDITVTIH
 KLVEGVKELYQANVATEQVNGKGFALKPQALLD TNWQKVI LRDKETQVR
 FTIDASQFSQKLKEQMANGYFLEGFVRFKAKDSNQELMSIPFVGNGDF
 ANLQALETPITYKLSKGSFYKPNDDTHKDQLEYNESAPFESNNYTALLT
 QSASWGVDYVKNNGEELAPESPKRIILGT FENKVEDKTIHLERDAAN
 NPYFAISPKNKGNDREITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
 YRKNFHNPNKQSDGHYRMDALQWSGLDKDGKVVADGFYTYRLRYTPVAEG
 ANSQESDFKVVSTKSPNLP SRAQFDETNRTLSLAMPKESYVPTYRLQL
 VLSHVVKDEEYGDETSYHYFHIDQEGKVTLPKTTVKIGESEVAVDPKALTL
 VVEDKAGNFATVKLSDLLNKAVVDEKENAIVISNSPKYFDNLKKEPMFIS
 KKEKVVNKNLEEIIILVKPQTTVTTQSLSKKEITKSGNEKVLSTNNSSRV
 AKIISPKNHGDVSNHTLPSTSDRATNGLFVGTLLALLSSLLLYLKPKKTKN
 NSK

GBS 147 also contains a C-terminal transmembrane and/or cytoplasmic region which may be located within the underlined sequence near the end of SEQ ID NO: 69 above. In one embodiment, one or more amino acids from the transmem-

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brane and/or cytoplasmic region are removed. An example of such a GBS 147 fragment is set forth below as SEQ ID NO: 71.

SEQ ID NO: 71

VDKHH SKKAILKLT LITTSILLMHSNQVNAEEQELKNQEQSPVEANVAQQ
 PSPSVTTNTVEKTSVTAASANTAKEMGDTSVKNDKTEDELLEELSKNLD
 10 TSNLGADLEEEYPSKPETTNNKESNVVINA STAIQKVPASAYEEVKPESK
 SSLAVLDTSKITKLQAITQRGKGNVVAIID TGF DINHDI FRLDSPKDDKH
 SFKTKTEFEELKAKHNITYGKWVNDKIVFAHNYANNNTETVADIAAMKDG
 15 YGSEAKNISHGTHVAGIFVGN SKRPAINGL LLEGAAPNAQVLLMRIPDKI
 DSDKFGEAYAKAITDAVNLGAKTINMSGKTADSLIALNDKVKLALKLAS
 EKGAVVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISEDLSVASYES
 LKTISEVVETTIEGKLVKLPIVTSKPFDKGKAYDVVYANYGAKKDFEGKD
 20 FKGKIALIERGGGLDFMTKI THATNAGVVGIVIFNDQEKRGNFILIPYREL
 PVGIIISKVDGERIKNTSSQLTFNQSFVVD SQGGNRMLEQSSWGVTAEAG
 IKPDVTASGFEIYSSYNNQYQTMSTGMA SPHVAGLMTMLQSHLAEKYK
 25 GMNLD SKKLELSKNI LMSSATALYSEEDKAFYSRQGGAGVDAEKAIQ
 AQYYITGNDGKAKINLKRMDKFDITVTIHKLVEGVKELYQANVATEQV
 NKGKGFALKPQALLD TNWQKVI LRDKETQVRFTIDASQFSQKLKEQMANGY
 30 FLEGFVRFKAKDSNQELMSIPFVGNGDFANLQALETPITYKLSKGSFY
 YKPNDDTHKDQLEYNESAPFESNNYTALLTQSASWGVDYVKNNGEEL
 PESPKRIILGT FENKVEDKTIHLERDAANNPYFAISPKNKGNDREITPQ
 35 ATFLRNVKDISAQVLDQNGNVIWQSKVLPSYRKNFHNPNKQSDGHYRMDA
 LQWSGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKVVSTKSPNLP
 SRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDETSYHYFH
 40 HIDQEGKVTLPKTTVKIGESEVAVDPKALTLVVEDKAGNFATVKLSDLLNK
 AVVDEKENAIVISNSPKYFDNLKKEPMFISKKEKVVNKNLEEIIILVKPQT
 TVTTQSLSKKEITKSGNEKVLSTNNSSRVAKIISPKNHGDVSNHT

In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic region are removed from the GBS 147 sequence. An example of such a GBS 147 fragment is set forth below as SEQ ID NO 72.

SEQ ID NO: 72

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTAASANTAKEMGDT
 55 SVKNDKTEDELLEELSKNLDTSNLGADLEEEYPSKPETTNNKESNVVINA
 STAIQKVPASAYEEVKPESKSSLAVLDTSKITKLQAITQRGKGNVVAIID
 TGF DINHDI FRLDSPKDDKHSFKTKTEFEELKAKHNITYGKWVNDKIVFA
 HNYANNNTETVADIAAMKDG YGSEAKNISHGTHVAGIFVGN SKRPAINGL
 60 LLEGAAPNAQVLLMRIPDKIDSDFGEAYAKAITDAVNLGAKTINMSGK
 TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDY
 GTVNSPAISEDLSVASYESLKTISEVVETTIEGKLVKLPIVTSKPFDKG
 KAYDVVYANYGAKDFEGKDFKGKIALIERGGGLDFMTKI THATNAGVVG

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IVIFNDQEKRGNFLIPYRELPGVIGISKVDGERIKNTSSQLTFNQSFVVD
 SQGGNRMLEQSSWGVTAEGAIKPDVTASGFEIYSSTYNNQYQTMSTGTSMA
 SPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK
 AFYSPRQQGAGVVD AEKAIQAQYYITGNDGKAKINLKRMDKFDITVTIH
 KLVEGVKELYQANVATEQVNGKGFALKPQALLDTNWQKVLIRDKETQVR
 FTIDASQFSQKLKEQMANGYFLEGFVRFEAKDSNQELMSIPFVGFNGDF
 ANLQALETPITYKLSKGSFYKPNDDTHKDQLEYNESAPFESNNYTALLT
 QASWGYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKTIHLERDAAN
 NPYFAISPNKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLP
 YRKNFHNPNKQSDGHYRMDALQWGLDKDKGVVADGPFYTYRLRYTPVAEG
 ANSQESDFKVQVSTKSPNLP SRAQFDETNRTLSLAMPKESYVPTYRLQL
 VLSHVVDKEEYDETSYHYPHIDQEGKVTLPKTVKIGESEVAVDPKALTL
 VVEDKAGNFATVKLSDLLNKAVVSEKENAIVISNSFKYFDNLKKEPMFIS
 KKEKVVNKNLEEIIILVKPQTTVTQSLSKETKSGNEKVLSTNNNSRV
 AKIISPKNHGD SVNHT

GBS 173

GBS 173 refers to an amidase family protein. Nucleotide and amino acid sequences of GBS 173 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 8787 and SEQ ID 8788. These sequences are set forth below as SEQ ID NOS 73 and 74:

SEQ ID NO. 73

ATGAAACGTAAATACTTTATTCTTAATACGGTGACGGTTTAAACGTTAGC
 TGCTGCAATGAATACTAGCAGTATCTATGCTAATAGTACTGAGACAAGTG
 CTTCACTAGTTCTACTACAAATACTATCGTTCAAATAAGTACAGTAAT
 CCTACCGCAAAATTTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGT
 AAAACAGATAAATCTCGCGCGCTTACAACAGTTGACACGCCTCATCATA
 TTTCACTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTCTGTTGAG
 AGTACTTCTACTAAGTTAACTGAAGAGACTTACAAACAAAAGATGGTCA
 AGATTTAGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACCTG
 TTAATATGGCATACTGATATTATTGCTAAAGAAAACCCATCTTTAAATGCA
 GTCACTACTACTAGACGCCAAGAGCTATTGAAGAGGCTAGAAAACCTAA
 AGATACCAATCAGCCGTTTTTAGGTGTCCCTGTGTAGTCAAGGGGTAG
 GGCACAGTATTAAAGTGGTGAAACCAATAATGGCTTGATCTATGCAGAT
 GGAAAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTT
 AGGATTTATTATTTTAGGACAAACGAACCTTCCAGAGTATGGGTGGCGTA
 ATATAACAGATTCTAAATTATACGGTCTAACGCATAATCCTTGGGATCTT
 GCTCATAATGCTGGTGGCTCTTCTGGTGGAAGTGACAGCAGCCATTGCTAG
 CGGAATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTA
 TTCCATCTTCTTGAGACGGGCTTGGTAGGTTAAAAACCAACAGAGGATTG
 GTGAGTAATGAAAGCCAGATTTCGTATAGTACAGCAGTTCAATTTCCATT
 AACTAAGTCATCTAGAGACGCAGAAACATTATTAAGTATCTAAAGAAA

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GCGATCAAACGCTAGTATCAGTTAATGATTAAAAATCTTACCAATTGCT
 TATACTTTGAAATCACCATGGGAACAGAGTTAGTCAAGATGCTAAAAA
 CGCTATTATGGACAACGTCACATTCTTAAGAAAACAGGATTCAAAGTAA
 CAGAGATAGACTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCA
 ACCTTGGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAAGACTT
 AAAAAACATGGTTTTACTAAGAAGACGTTGATCCTATTACTTGGGCAG
 TTCATGTTATTATCAAAATTCAGATAAGGCTGAACCTAAGAAATCTATT
 ATGGAAGCCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCT
 TCACAAGCAATTTCTATTCTTCTATCGCCACGACCGCAAGTTTAGCCC
 CTCTAAATACAGATCCATATGTAACAGAGGAAGATAAAAAGAGCGATTAT
 AATATGGAAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTTAATCGCCA
 GTGGGAGCCTATGTTGCGTAGAACACCTTTTACACAATGCTAATATGA
 CAGGACTCCGAGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTA
 CCCATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAA
 TAAATTTGCAACTTTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGC
 AAAGAATAATAGATAAAGAAGTGAAACCATCTACTGGCCTAATACAGCCT
 ACTAACTCCCTCTTTAAAGCTCATTATCATTAGTAAATTTAGAAGAAAA
 TTCACAAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTG
 TTAAAAATAAACCATCCGTAATGGCATATCAAAAGCACTTCTCTAAACA
 GGTGATACAGAATCAAGCCTATCTCCAGTTTTAGTAGTAACCCCTTTTATT
 AGCTTGTTTTAGCTTTGTAACAAAAAGAATCAGAAAAAGT

SEQ ID NO. 74

MKRKYFILNTVTVLTLAAAMNTSSIIYANSTETSASVVPTTNTIVQNTDSN
 PTAKFVSESGQSVIGQVKPDNSAALTTVDTPHHISAPDALKTTQSSPVVE
 STSTKLTEETYKQKDGQDKANMVRSGQVTS EELVNMAYDIIAKENPSLNA
 VITTRRQEAIEEARLKDNTNQPFGLVPLLVKGLGHSIKGGETTNNGLIYAD
 GKISTFDSSYVKKYKDLGFIILGQTNFPEYGRWNITDSKLYGLTHNPWDL
 AHNAGSSSGSAAAIASGMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGL
 VSNEKPDSSYSTAVHFPLTKSSRDAETLLTYLKKVDQTLVSVNDLKLPIA
 YTLKSPMGTEVSQDAKNAIMDNVTF LRKQGFVTEIDLPI DGRALMRDYS
 TLAIGMGAGSTIEKDLKKHGFTKEDVDPI TWAVHVIYQNSDKAELKKS I
 MEAQKHMDYRKAMEKLHKQFPPIFLSPPTASLAPLNTDPYVTEEDKRAIY
 NMENLSQEERIALFNRQWEPMLRPTPTQIANMTGLPAISIPTYLSESL
 PIGTMLMAGANYDMVLIKFATPFKHHGFNVKQRIIDKEVKPSTGLIQP
 TNSLFPKAHSSLVNLEENSQVTQVSISKWMKSSVKNKPSVMAYQKALPKT
 GDTESLSFVLVVTLLACFSFVTKKNQKS

GBS 173 contains an N-terminal leader or signal sequence region which is indicated by the underlined sequences at the beginning of SEQ ID NO: 74 above. In one embodiment, one or more amino acids from the leader or signal sequence of GBS 173 are removed. An example of such a GBS 173 fragment is set forth below as SEQ ID NO: 75.

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SEQ ID NO: 75
 TTNTIVQTNSNPTAKFVSESGQSVIGQVKPDNSAALTTVDPHHISAPD
 ALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMA
 DIIAKENPSLNAVITTRRQEAIEEARKLKDTNQPFGLVPLLVKGLGHSIK
 GGETNNGLIYADGKISTFDSSYVKYKDLGFIILGQTNFPEYGWRNITDS
 KLYGLTHNPWDLAHNAGGSSGGSAAAIAASGMTPIASGSDAGGSIRIPSSW
 TGLVGLKPTRGLVSNKPDYSYSTAVHFPLTKSSRDAETLLTYLKKSDQTL
 VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDL
 PIDGRALMRDYSTLAIGMGAGSTIEKDLKKHGFTKEDVDPITWAVHVIY
 QNSDKAELKKSI MEAQKHMDDYRKAMEKLHKQFPFIPLSPTTASLAPLNTD
 PYVTEEDKRAIYNMENLSQEERIALFNRQWEPMLRRTPTQIANMTGLPA
 ISIPTYLSESGLPITMLMAGANYDMVLKIFATFFEKHHGFNVKQRIID
 KEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSISSKWMKSSVKNK
 SVMAYQKALPKTGDESSLSPVLVVTLLAVFSFVTKKNQKS

GBS 173 may also contain a C-terminal transmembrane and/or cytoplasmic region which may be located within the underlined region near the end of SEQ ID NO: 74 above. In one embodiment, one or more amino acids from the transmembrane or cytoplasmic region of GBS 173 are removed. An example of such a GBS 173 fragment is set forth below as SEQ ID NO: 76.

SEQ ID NO: 76
 MKRKYFILNTVTVTLTAAAMNTSSIIYANSTETSASVVPNTNTIVQTNSN
 PTAKFVSESGQSVIGQVKPDNSAALTTVDPHHISAPDALKTTQSSPVVE
 STSTKLTEETYKQKDGQDKANMVRSGQVTSEELVNMAVDIIAKENPSLNA
 VITTRRQEAIEEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYAD
 GKISTFDSSYVKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDL
 AHNAGGSSGGSAAAIAASGMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGL
 VSNKPDYSYSTAVHFPLTKSSRDAETLLTYLKKVDQTLVSVNDLKSLPIA
 YTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDLPIIDGRALMRDYS
 TLAIGMGAGSTIEKDLKKHGFTKEDVDPITWAVHVIYQNSDKAELKKSI
 MEAQKHMDDYRKAMEKLHKQFPFIPLSPTTASLAPLNTDPYVTEEDKRAIY
 NMENLSQEERIALFNRQWEPMLRRTPTQIANMTGLPAISIPTYLSESGLP
 IGTMLMAGANYDMVLKIFATFFEKHHGFNVKQRIIDKEVKPSTGLIQP
 TNSLFAHSSLVNLEENSQVTQVSISSKWMKSSVKNK

In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic region are removed. An example of such a GBS 173 fragment is set forth below as SEQ ID NO: 77.

SEQ ID NO: 77
 TTNTIVQTNSNPTAKFVSESGQSVIGQVKPDNSAALTTVDPHHISAPD
 ALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMA
 DIIAKENPSLNAVITTRRQEAIEEARKLKDTNQPFGLVPLLVKGLGHSIK

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GGETNNGLIYADGKISTFDSSYVKYKDLGFIILGQTNFPEYGWRNITDS
 KLYGLTHNPWDLAHNAGGSSGGSAAAIAASGMTPIASGSDAGGSIRIPSSW
 5 TGLVGLKPTRGLVSNKPDYSYSTAVHFPLTKSSRDAETLLTYLKKSDQTL
 VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVKTEIDL
 PIDGRALMRDYSTLAIGMGAGSTIEKDLKKHGFTKEDVDPITWAVHVIY
 10 QNSDKAELKKSI MEAQKHMDDYRKAMEKLHKQFPFIPLSPTTASLAPLNTD
 PYVTEEDKRAIYNMENLSQEERIALFNRQWEPMLRRTPTQIANMTGLPA
 ISIPTYLSESGLPITMLMAGANYDMVLKIFATFFEKHHGFNVKQRIID
 15 KEVKPSTGLIQPTNSLFAHSSLVNLEENSQVTQVSISSKWMKSSVKNK

GBS 313

Nucleotide and amino acid sequences of GBS 313 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 4089 and SEQ ID 4090. These sequences are set forth as SEQ D NOS 78 and 79 below:

SEQ ID NO. 78
 25 ATGAAACGTATTGCTGTTTAACTAGTGGTGGTGACGCCCTGGTATGAA
 CGCTGCTATCCGTGCAGTTGTTTCGTAAAGCAATTTCTGAAGGTATGGAAG
 TTTACGGCATCAACCAAGGTTACTATGGTATGGTGACAGGGGATATTTTC
 CCTTTGGATGCTAATCTGTTGGGGATACTATCAACCGTGGAGGAACGTT
 30 TTTACGTTTCAGCACGTTATCCTGAATTTGCTGAACTGAAGGTACAGCTTA
 AAGGGATTGAACAGCTTAAAAAACACGGTATTGAAGGTGTAGTAGTTATC
 GGTGGTGTATGGTCTTATCATGGTGTCTATGCGTCTAACTGAGCACGGTTT
 35 CCCAGCTGTTGGTTTGCCGGGTACAATTGATAACGATATCGTTGGCACTG
 ACTATACTATTGGTTTTCACACAGCAGTTGCAGACAGCAGTTGAGAATCTT
 GACCGTCTTCGTGATACATCAGCAAGTCATAACCGTACTTTTGTGTTGA
 40 GGTATGGGAAGAAATGCAGGAGATATCGCTCTTTGGTCAGGTATCGCTG
 CAGGTGCAGATCAAATTATGTTCTGAAGAAGAGTTCAATATTGATGAA
 GTTGCTCAAATGTTAGAGCTGGCTATGCAGCTGGTAAACATCACCAAAT
 45 CATCGTCCTTGCAAGAGGTGTTATGAGTGGTGATGAGTTTGCAAAACAA
 TGAAAGCAGCAGGAGACGATAGCGATCTTCGTGTGACGAATTTAGGACAT
 CTGCTCCGTGGTGGTAGTCCGACGGCTCGTGATCGTGTCTTAGCATCTCG
 50 TATGGGAGCGTACGCTGTTCAATTGTTGAAAGAAGGTCTGGTGGTTTAG
 CCGTTGGTGTCCACACGAAGAAATGGTTGAAAGTCCAATTTTAGGTTTA
 GCAGAAGAAGGTGCTTTGTTGAGCTTGACTGATGAAGGAAAAATCGTTGT
 55 TAATAATCCGCATAAAGCGGACCTTCGCTTGGCAGCACTTAATCGTGACC
 TTGCCAACCAAGTAGTAA

SEQ ID NO. 79
 MKRIAVLTSGGDAPGMNAAIRAVVRKAISEGMEVYGINQGYGMVTGDIF
 60 PLDANSVGDTINRGGTFLRSARYPEFAELEGQLKIEQLKKHIGIEGVVVI
 GGDGSYHGAMRLTEHGFPVAVGLPGTIDNDIVGTDYITGFDTAVATAVENL
 DRLRDTASASHNRTFVVEVMGRNAGDIALWSGIAAGADQIIVPEEENIDE
 65 VVSNVRAGYAAGKHHQIIVLAEGVMSGDEFKTMKAAGDSDSLRVTLNLGH

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LLRGGSPRTARDVRLASRMGAYAVQLLKEGRGGLAVGVHNEEMVESPI LGL
AEEGALFSLTDEGKIVVNNPHKADLR LALNRDLANQSSK

GBS 328

GBS 328 belongs to the 5'-nucleotidase family. Nucleotide and amino acid sequences of GBS 328 sequenced from sero-type V isolated strain 2603 V/R are set forth in Ref. 2 as SEQ ID 6015 and SEQ ID 6016. These sequences are set forth below as SEQ ID NOS 80 and 81:

SEQ ID NO. 80

ATGAAAAAGAAAATTATTTTGAAAAGTAGTGTTCTTGGTTTAGTCGCTGG
GACTTCTATTATGTTCTCAAGCGTGTTGCGGACCAAGTCGGTGCTCAAG
TTATAGGCGTCAATGACTTTCATGGTGCACTTGACAATACTGGAACAGCA
AATATGCCTGATGAAAAAGTTGCTAATGCTGGTACTGCTGCTCAATTAGA
TGCTTATATGGATGACGCTCAAAAAGATTTCAACAACTAACCTTAATG
GTGAAAGCATTAGGGTTCAAGCAGCGCATATGGTTGGAGCAAGTCCAGCC
AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTTAATGCAAT
GAATGTTGAGTATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGG
CAGAATATAATCGTATCGTTACTGGTAAAGCCCTGCTCCAGATTCTAAT
ATTAATAATATTACGAAATCATACCCACATGAAGCTGCAAAACAAGAAAT
TGTAAGTGGCAAAATGTTATTGATAAAGTTAACAACAAATTCCTTACAATT
GGAAGCCTTACGTATTAAAAATATTCCTGTAAATAACAAAAGTGTGAAC
GTTGGCTTTATCGGGATTGTGACCAAGACATCCCAACCTTGTCTTACG
TAAAAATTATGAACAATATGAATTTTGTAGTGAAGCTGAACAATCGTTA
AATACGCCAAGAATTACAAGCTAAAAATGTCAAAGCTATTGTAGTTCTC
GCACATGTACCTGCAACAAGTAAAAATGATATTGCTGAAGGTGAAGCAGC
AGAAATGATGAAAAAGTCAATCAACTCTCCCTGAAATAGCGTAGATA
TTGTCTTTGCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGTGATGTACG
TGGTGTCTTAGATACTGATACACAAGATTTCAATTGAGACCCCTTCAGCTA
AAGTAATTGCAGTTGCTCCTGGTAAAAAACAGGTAGTGCCGATATTCAA
GCCATTGTTGACCAAGCTAATACTATCGTTAAACAAGTAACAGAAGCTAA
AATTGGTACTGCCGAGGTAAGTGTGATGATTACGCGTTCTGTTGATCAAG
ATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATT
GCTCGAAAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGG
CATTCTGCTGACTTACTCATCAACACAGATGGAACAATCACCTGGGGAG
CTGCACAAGCAGTTCAACCTTTTGGTAAATCTTACAAGTCTGCGAAAT
ACTGGTAGAGATCTTTATAAGCACTCAACGAACAATACGACCAAAAACA
AAATTTCTCTCTCAATAGCTGGTCTGCGATACACTTACACAGATAATA
AAGAGGGCGGGGAAGAACACCATTAAAGTTGTAAAGCTTATAAATCA
AATGGTGAGGAAATCAATCCTGATGCAAAATACAAATTAGTTATCAATGA
CTTTTATTCTGGTGGTGGTATGGCTTGCAAGCTTCAGAAATGCCAAC
TTCTAGGAGCCATTAAACCCGATACAGAGGTATTATGGCCTATATCACT

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GATTTAGAAAAAGCTGGTAAAAAGTGAGCGTTCCAAATAATAAACCTAA
AATCTATGTCACTATGAAGATGGTTAATGAACTATTACACAAAATGATG
5 GTACACATAGCATTATTAAGAACTTTATTAGATCGACAAGGAAATATT
GTAGCACAAGAGATTGTATCAGACACTTTAAACCAACAAAATCAAATC
TACAAAAATCAACCTGTAACTACAATTACAAAAACAATTACACCAAT
10 TTACAGCTATTAAACCTATGAGAAATTATGGCAACCATCAAACCTCACT
ACTGTAAATCAAAACAATTACAAAAACAACCTCTGAATATGGACAATC
ATTCCTTATGTCTGTCTTTGGTGTGGACTTATAGGAATTGCTTTAATA
15 CAAAGAAAAACATATGAAA

SEQ ID NO. 81

MKKKII LKSSVLGLVAGTSI MFSSVFADQVGVQVIGVND F HGALDNTGTA
NMPDGKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPA
20 NSGLLQDEPTVKNFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAPDSN
INNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKP YAIKNIPVNNKSVN
VGFIGIVTKDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIIVL
25 AHVPATSKNDIAEGEAAEMMKVNQLFPENSVDIVFAGHNHQYTNGLVGK
TRIVQALSQ GKAYADVRGVLDTDTQDFIETPSAKVIAPGKKTGSADIQ
AIVDQANTIVKQVTEAKIGTAEVSVMITRSVDQDNVSPVGS LITEAQLAI
30 ARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQFPFNILQVVEI
TGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKS
NGEENPD AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYIT
35 DLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQNGNI
VAQEIVSDTLNQTKSKTKINPVTTIHKQLHQFTAINPMRNYGKPSNST
TVKSKQLPKTNSEYGQSFLMSVFGVGLIGIALNTKKKHKMK

GBS 328 may contain an N-terminal leader or signal sequence region which is indicated by the underlined sequence at the beginning of SEQ ID NO: 81 above. In one embodiment, one or more amino acids from the leader or signal sequence region of GBS 328 are removed. An example of such a GBS 328 fragment is set forth below as SEQ ID NO: 82.

SEQ ID NO: 82

HGALDNTGTANMPDGKVANAGTAAQLDAYMDDAQKDFDQTNPNGESIRVQ
50 AGDMVGASPANSGLLQDEPTVKNFNAMNVEYGT LGNHEFDEGLAEYNRIV
TGKAPAPDSNINNITKSY PHEAAKQEI VVANVIDKVNKQI PYNWKP YAIK
NIPVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEAETIVKYAKELQ
55 AKNVKAIIVLHVHPATSKNDIAEGEAAEMMKVNQLFPENSVDIVFAGHN
HQYTNGLVGKTRIVQALSQ GKAYADVRGVLDTDTQDFIETPSAKVIAPV
GKKTGSADIQ AIVDQANTIVKQVTEAKIGTAEVSVMITRSVDQDNVSPVG
60 SLITEAQLAIARRKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQVQP
FGNQLQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEET
PFKVVKAYKSGEENPD AKYKLVINDFLFGGGDGFASFRNAKLLGAINP
65 DTEVFMAYITDLEKAGKKVSVPNKPKIYVTMKNVNETITQNDGTHSIIK

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KLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTHKKQLHQFTAINPM
RNYGKPSNSTTVKSKQLPKTNSEYQSFMLSVFVGLIGIALNTKKHMK

GBS 328 may also contain a transmembrane and/or cytoplasmic domain region. In one embodiment, one or more amino acids from the transmembrane and/or cytoplasmic domain region of GBS 328 are removed. An example of such a GBS 328 fragment is set forth below as SEQ ID NO: 83.

SEQ ID NO: 83

MKKKIIILKSSVLGLVAGTSIMFSSVFADQVGVQVIGVNDHFHGLDNTGTA
NMPDGKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGASPA
NSGLLQDEPTVKNFNAMNVEYGT LGNHEFDEGLAEYNRIVTGKAPAPDSN
INNI TKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIKINIPVNNKSVN
VGFIGIVTKDIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAIIVVL
AHVPATSKNDIAEGEAAEMMKVNLFPENSVDIVFAGHNHQYTNGLVGK
TRIVQALSQKAYADVRGVLDTDQDFIETPSAKVIAVAPGKKTGSADIQ
AIVDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSPVGLITEAQLAI
ARKSWPIDIFAMTNNGGIRADLLIKPDGTITWGAAQAVQPPGNILQVVEI
TGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKS
NGEENPDAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIYT
DLEKAGKKVSPNNKPKIYVTMKNVNETITQNDGTHSIIKKLYLDRQGN
IVAQEIVSDTLNQTKSKSTKINPVTTHKKQLHQFTAINPMRNYGKPSNST
TVKS

In one embodiment, one or more amino acids from the leader or signal sequence region and one or more amino acids from the transmembrane or cytoplasmic region of GBS 328 are removed. An example of such a GBS 328 fragment is set forth below as SEQ ID NO: 84.

SEQ ID NO: 84

HGALDNTGTANMPDGKVANAGTAAQLDAYMDDAQKDFDQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKNFNAMNVEYGT LGNHEFDEGLAEYNRIV
TGKAPAPDSNINNI TKSYPHEAAKQEIVVANVIDKVNKQIPYNWKPYAIK
NIPVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEAETIVKYAKELQ
AKNVKAIIVLAHVPAATSKNDIAEGEAAEMMKVNLFPENSVDIVFAGHN
HQYTNGLVGKTRIVQALSQKAYADVRGVLDTDQDFIETPSAKVIAVAP
GKKTGSADIQAIIVDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSPV
GLITEAQLAIARRKSWPIDIFAMTNNGGIRADLLIKPDGTITWGAAQVQ
FGNIIQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEET
PFKVVKAYKNGEENPDAKYKLVINDFLFGGGDGFASFRNAKLLGAINP
DTEVFMAIYTDLEKAGKKVSPNNKPKIYVTMKNVNETITQNDGTHSIIK
KLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTHKKQLHQFTAINPM
RNYGKPSNSTTVKS

GBS 656

GBS 656 refers to a putative DNA-entry nuclease. Nucleotide and amino acid sequences of GBS 656 sequenced from serotype V isolated strain 2603 V/R are set forth in Ref. 2 as

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SEQ ID 9323 and SEQ ID 9324. These sequences are set forth below as SEQ ID NOS 85 and 86:

SEQ ID NO. 85

5 ATGAAAAGATTACATAAACTGTTTATAACCGTAATTGCTACATTAGGTAT
GTTGGGGGTAATGACCTTTGGTCTTCCAACGCGAGCCGCAAAACGTAACGC
CGATAGTACATGCTGATGTCAATTCATCTGTTGATACGAGCCAGGAATTT
10 CAAAATAATTTAAAAAATGCTATTGGTAACCTACCATTTCAATATGTTAA
TGGTATTTTATGAATTAATAATAATCAGACAAATTTAAATGCTGATGTCA
ATGTTAAAGCGTATGTTCAAAATACAATTGACAATCAACAAAGACTATCA
15 ACTGCTAATGCAATGCTTGATAGAACCATTTCGTCATATCAAAATCGCAG
AGATACCACTCTTCCCGATGCAAAATGGAAACCATTAGGTTGGCATCAAG
TAGCTACTAATGACCATTATGGACATGCAGTCGACAAGGGGCATTTAATT
20 GCCTATGCTTTAGCTGGAATTTCAAAGGTTGGGATGCTTCCGTGTCAAA
TCCTCAAAATGTTGTACACAAAACAGCTCATTTCAACCAATCAAAATCAAA
AAATCAATCGTGGACAAAATTATTTGAAAGCTTAGTTCGTAAGCGCGTT
25 GACCAAAACAAACGCTGTTTCGTTACCGTGTAACTCCATTGTACCGTAATGA
TACTGATTTAGTTCATTTGCAATGCACCTAGAACGTAATCACAAGATG
GCACATTAGAATTTAATGTTGCTATTCCAAACACACAAGCATCATACT
30 ATGGATTATGCAACAGGAGAAATAACACTAAAT

SEQ ID NO. 86

MKRLHKLFIITVIATLGMGLVMTFGLPTQPNVPIVHADVNSSVDSQEF
QNNLKNAINLPPFYVNGIYELNNNQTNLNDVNVKAYVQNTIDNQRLS
35 TANAMLDRTIRQYQNRDITLDPANWKPLGWHQVATNDHYGHAVDKGHLI
AYALAGNFKGWDASVSNPNQNVVTQTAHSNQSNQKINRGQNYYESLVRKAV
DQNKVRVRYRVTPLRYNDTDLVPFAMHLEAKSQDGTLEFNVAIPNTQASYT
40 MDYATGEITLN

GBS 67

The following offers examples of preferred GBS 67 fragments. Nucleotide and amino acid sequence of GBS 67 sequences from serotype V isolated strain 2603 are set forth below as SEQ ID NOS: 87 and 88.

SEQ ID NO: 87

50 ATGAGAAAAATACCAAAATTTTCTAAAATATTGACGTTAAGTCTTTTGT
TTTGTGCGAAATACCGCTTAATACCAATGTTTGTAGGGGAAAGTACCGTAC
CGGAAAAATGGTGCTAAAGGAAAGTTAGTTGTTAAAAAGACAGATGACCAG
AACAAACCACTTTCAAAGCTACCTTTGTTTAAAACTACTGCTCATCC
55 AGAAAGTAAATAGAAAAAGTAAGTCTGAGCTAACAGGTGAAGCTACTT
TTGATAATCTCATACCTGGAGATTATACCTTTATCAGAAGAAACAGCGCCC
GAAGGTTATAAAAGACTAACAGACTTGGCAAGTTAAGGTTGAGAGTAA
60 TGGAAAACTACGATACAAAATAGTGGTGATAAAAAATTCACAATTGGAC
AAAAATCAGGAAGAACTAGATAAGCAGTATCCCCCACAGGAATTTATGAA
GATACAAAGGAATCTTATAAACTTGAGCATGTTAAAGGTTCAAGTTCCAAA
65 TGGAAAGTCAGAGGCAAAAGCAGTTAACCCATATTCAAGTGAAGGTGAGC

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ATATAAGAGAAATTCAGAGGGAACATTATCTAAACGTATTTTCAGAAGTA
 GGTGATTAGCTCATAATAAATATAAAATTGAGTTAACTGTCAGTGGA
 AACCATAGTAAACCAGTGGACAAACAAAAGCCGTTAGATGTTGCTTCG
 TACTCGATAATTCTAACTCAATGAATAACGATGGCCCAAATTTTCAAAGG
 CATAATAAGCCAAGAAAGCTGCCGAAGCTCTTCGACCGCAGTAAAGA
 TATTTTAGGAGCAACAGTGATAATAGGGTGCATTAGTTACCTATGGTT
 CAGATATTTTGTAGGTAGGAGTGTAGATGTCGTAAGGATTAAAGAA
 GATGATAAATATTATGGCCTTCAAACTAAGTTCACAATTCAGACAGAGAA
 TTATAGTCATAACAATTAACAAATAATGCTGAAGAGATTATAAAAGGA
 TTCCGACAGAAGCTCCTAAAGCTAAGTGGGATCTACTACCAATGGATTA
 ACTCCAGAGCAACAAAAGGAGTACTATCTTAGTAAAGTAGGAGAAACATT
 TACTATGAAAGCCTTCATGGAGGAGATGATATTTTGGTCAAGTAAATC
 GAAATAGTCAAAAAATTATTGTTTCATGTAAGTGGTGTTCCTACGAGA
 TCATATGCTATTATAAATTTTAACTGGGTGCATCATATGAAAGCCAATT
 TGAACAAATGAAAAAATGATATCTAAATAAAAGTAATTTTCTACTTA
 CTGATAAGCCCGAGGATATAAAAGGAAATGGGGAGAGTTACTTTTTGTTT
 CCCTTAGATAGTTATCAAAACAGATAATCTCTGGAACTTACAAAACT
 TCATTATTTAGATTTAAATCTTAATTACCCTAAAGGTACAATTTATCGAA
 ATGGACCAGTGAAAGAACATGGAACACCAACCAAACTTTATATAAATAGT
 TTAAACAGAAAAATTATGACATTTTAAATTTTGGTATCGATATATCTGG
 TTTTAGACAAGTTTATAATGAGGAGTATAAGAAAAATCAAGATGGTACTT
 TTCAAAAATTGAAAGAGGAAGCTTTTAAACTTTTCAAGATGGAGAAATCACA
 GAACTAATGAGGTCGTCTCTTCCAAACCTGAGTACTACACCCCTATCGT
 AACTTCAGCCGATACATCTAACAATGAAATTTTATCTAAAATTGAGCAAC
 AATTTGAAACGATTTTAAACAAAAGAAAACCAATTGTTAATGGAACATC
 GAAGATCCTATGGGTGATAAAATCAATTTACAGCTTGGTAATGGACAAAC
 ATTACAGCCAAGTGATTATACTTTACAGGGAATGATGGAAGTGAATGA
 AGGATGGTATTGCAACTGGTGGGCCTAATAATGATGGTGGAATACTTAAG
 GGGGTAAATTAGAATACATCGGAAATAAACTCTATGTTAGAGTTTGAA
 TTTAGGAGAAGGTCAAAAAGTAACACTCACATATGATGTGAAACTAGATG
 ACAGTTTATAAGTAACAAATCTATGACACTAATGGTAGAACAAACATTG
 AATCCTAAGTCAGAGGATCCTAATACACTTAGAGATTTTCCAATCCCTAA
 AATTCGTGATGTGAGAGAATATCTACAATAACGATTAAAAACGAGAAGA
 AGTTAGGTGAAATGAATTTATAAAAGTTGATAAAGATAATAAAGTTG
 CTCTCAAGGAGCTACGTTTGAACCTCAAGAATTTAATGAAGATTATAA
 ACTTTATTTACCAATAAAAAATAAATTCAAAAGTAGTGACGGAGAGAA
 ACGGCAAAATTTCTTACAAGATTTGAAAGATGGCAAAATATCAGTTAATA
 GAAGCAGTTTCGCGGAGGATTATCAAAAATTTACTAATAAACCAATTTT
 AACTTTTGAAGTGGTTAAAGGATCGATAAAAAATATAATAGCTGTTAATA
 AACAGATTTCTGAATATCATGAGGAAGGTGACAAGCATTTAATTACCAAC
 ACGCATATTTCCACCAAAAGGAATTATCTCTATGACAGGTGGAAAGGAAT

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TCTATCTTTTCATTTTAATAGGTGGAGCTATGATGTCTATTGCAGGTGGAA
 TTTATATTTGGAAAAGGTATAAGAAATCTAGTGATATGTCCATCAAAAAA
 5 GAT
 SEQ ID NO: 88
 MRKYQKFSKILTLSLFCLSQIPLNTNVLGESTVPENGAKGLVVKKTDQ
 10 NKPLSKATFVLKTTAHPEKIEKVTAULTGEATFDNLIPGDYTLSEETAP
 EGYKKTNTQWQVKVESNGKTTIQNSGDKNSTIGQNQEELDKQYPPTGIYE
 DTKESYLKEHVKGSPNGKSEAKAVNPYSSEGEHIREIPEGLSKRISSEV
 15 GDLAHNKYKIELTVSGKTIKPVQKQKPLDVVFLDNSNSMNDGPNFQR
 HNKAKKAAEALGTAVKDI LGANSNDRVALVTYGSDFDGRSDVVVKGFKE
 DDKYGLQTKFTIQTENYSHKQLTNNABEIIKRIPTAEPKAKWGSTTNGL
 20 TPEQQKEYYLSKVGETFTMKAFMEADDILSQVNRNSQKIIVHVDGVPTR
 SYAINNFKLGASYESQGEQMKNGYLNKSNFLITDKPEDIKNGESYFLF
 PLDSYQTQIIISGNLQKLHYLDLNLNYPKGTIYRNGPVKEHGTPTKLYINS
 LKQKNYDIFNFGIGISGFRQVYNEEYKKNQDGTQKLKEEAFKLSDEGIT
 25 ELMRSFSSKPEYYTPIVTSADTSNNEILSKIQQQFETILTKENSIVNGTI
 EDPMGDKINQLGNGQTLQPSDYTLQGNDGSVMKDIATGGPNNDGGILK
 GVKLEYIGNKLYVRGLNLGEGQKVTLYDVKLDDSFISNKFYDNGRTTL
 30 NPKSEDPNTLRDFPIPKIRDVREYPTITIKNEKKLGEIEFIKVDKDNKLL
 LLKGATFELQEFNEDYKLYPIKNNSKVVVTGENGKISYKDLKDGKYLII
 EAVSPEDYQKINTKPILTFEVVKSGIKNIIAVNKQISEYHEEGDKHLITN
 35 THIPKGIIPMTGGKGILS FILIGGAMMSIAGGIYIWKRYKSSDMSI
 KKD

GBS 67 contains a C-terminus transmembrane region
 which is indicated by the underlined region closest to the
 C-terminus of SEQ ID NO: 88 above. In one embodiment;
 one or more amino acids from the transmembrane region is
 removed and or the amino acid is truncated before the trans-
 membrane region. An example of such a GBS 67 fragment is
 set forth below as SEQ ID NO: 89.

SEQ ID NO: 89
 MRKYQKFSKILTLSLFCLSQIPLNTNVLGESTVPENGAKGLVVKKTDQ
 50 NKPLSKATFVLKTTAHPEKIEKVTAULTGEATFDNLIPGDYTLSEETAP
 EGYKKTNTQWQVKVESNGKTTIQNSGDKNSTIGQNQEELDKQYPPTGIYE
 DTKESYLKEHVKGSPNGKSEAKAVNPYSSEGEHIREIPEGLSKRISSEV
 55 GDLAHNKYKIELTVSGKTIKPVQKQKPLDVVFLDNSNSMNDGPNFQR
 HNKAKKAAEALGTAVKDI LGANSNDRVALVTYGSDFDGRSDVVVKGFKE
 DDKYGLQTKFTIQTENYSHKQLTNNABEIIKRIPTAEPKAKWGSTTNGL
 60 TPEQQKEYYLSKVGETFTMKAFMEADDILSQVNRNSQKIIVHVDGVPTR
 SYAINNFKLGASYESQGEQMKNGYLNKSNFLITDKPEDIKNGESYFLF
 PLDSYQTQIIISGNLQKLHYLDLNLNYPKGTIYRNGPVKEHGTPTKLYINS
 LKQKNYDIFNFGIGISGFRQVYNEEYKKNQDGTQKLKEEAFKLSDEGIT
 65 ELMRSFSSKPEYYTPIVTSADTSNNEILSKIQQQFETILTKENSIVNGTI

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EDPMGDKINLQLGNGQTLQPSDYTLQGNDGSVMKDGATGGPNNDGGILK
GVKLEYIGNKLYVRGLNLGEGQKVTLTLYDVKLDDSFISNKFYDTNGRTTL
NPKSEDPNTLRDFFPIPKIRDVREYPTITIKNEKKLGEIEFIKVDKDNKKL
LLKGATFELQEFNEDYKLYPIKNNNSKKVVTGENGKISYKDLKDGKYQLI
EAVSPEDYQKITNKPILTFEVVKGSIKNIIAVNKQISEYHEEGDKHLITN
THIPPKGIIPMTGGKGILS

GBS 67 contains an amino acid motif indicative of a cell wall anchor (an LPXTG motif) (SEQ ID NO:93): SEQ ID NO: 90 IPMTG. (shown in italics in SEQ ID NO: 88 above). In some recombinant host cell systems, it may be preferable to remove this motif to facilitate secretion of a recombinant GBS 67 protein from the host cell. Accordingly, in one preferred fragment of GBS 67 for use in the invention, the transmembrane and the cell wall anchor motif are removed from GBS 67. An example of such a GBS 67 fragment is set forth below as SEQ ID NO: 91.

SEQ ID NO: 91

MRKYQKFSKILTLTLFCLSQIPLNTNVLGESTVPENGAKGLVVKKTDDQ
NKPLSKATFVLKTAHPESKIEKVTAILTGEATFDNLIPGDTLSEETAP
EGYKKTNTQTQVKVESNGKTTIQNSGDKNSTIGQNQEELDKQYPTGIYE
DTKESYLKEHVKGVSVPNGKSEAKAVNPYSSEGEHIREIPEGTLSKRISEV
GDLAHNKYKIELTVSGKTIKVPVDKQKPLDVVFLDNSNSMNDGNPQFR
HNKAKAAEALGTAVKIDILGANSNDRVALVTYGSDFDGRSVDVVGKFKE
DDKYGLQTKFTIQTENYSHKQLTNNAEEIIKRIPTAPKAKWGSTTNGL
TPEQQKEYYLSKVGETFTMKAFMEADDILSQVNRNSQKIIHVHTDGVPTR
SYAINNFKLGASYESQGEQMKNGYLNKSNFLLTDKPEDIKNGESYFLF
PLDSYQTQIIISGNLQKLHYLDLNLNYPKGTIYRNGPVKEHGTPTKLYINS
LKQKNYDIFNFGIGISGFRQVYNEEYKKNQDGTQKLKEEAFKLSDGEIT
ELMRFSSSKPEYYTPIVTSADTSNNEILSKIQQQFETILTENSIVNGTI
EDPMGDKINLQLGNGQTLQPSDYTLQGNDGSVMKDGATGGPNNDGGILK
GVKLEYIGNKLYVRGLNLGEGQKVTLTLYDVKLDDSFISNKFYDTNGRTTL
NPKSEDPNTLRDFFPIPKIRDVREYPTITIKNEKKLGEIEFIKVDKDNKKL
LLKGATFELQEFNEDYKLYPIKNNNSKKVVTGENGKISYKDLKDGKYQLI
EAVSPEDYQKITNKPILTFEVVKGSIKNIIAVNKQISEYHEEGDKHLITN
THIPPKGI

The compositions of the invention may also include combinations including one or more known GBS antigens in combination with GBS 80.

There is an upper limit to the number of GBS antigens which will be in the compositions of the invention. Preferably, the number of GBS antigens in a composition of the invention is less than 20, less than 19, less than 18, less than 17, less than 16, less than 15, less than 14, less than 13, less than 12, less than 11, less than 10, less than 9, less than 8, less than 7, less than 6, less than 5, less than 4, or less than 3. Still more preferably, the number of GBS antigens in a composition of the invention is less than 6, less than 5, or less than 4. Still more preferably, the number of GBS antigens in a composition of the invention is 3.

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The GBS antigens used in the invention are preferably isolated, i.e., separate and discrete, from the whole organism with which the molecule is found in nature or, when the polynucleotide or polypeptide is not found in nature, is sufficiently free of other biological macromolecules so that the polynucleotide or polypeptide can be used for its intended purpose.

Fusion Proteins

The GBS antigens used in the invention may be present in the composition as individual separate polypeptides, but it is preferred that at least two (i.e. 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) of the antigens are expressed as a single polypeptide chain (a "hybrid" or "fusion" polypeptide). Such fusion polypeptides offer two principal advantages: first, a polypeptide that may be unstable or poorly expressed on its own can be assisted by adding a suitable fusion partner that overcomes the problem; second, commercial manufacture is simplified as only one expression and purification need be employed in order to produce two polypeptides which are both antigenically useful.

The fusion polypeptide may comprise two or more polypeptide sequences from the group consisting of GBS 80, GBS 91, GBS 104, GBS 184, GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361, GBS 404, GBS 690 and GBS 691. Preferably, the polypeptide sequences are selected from the group consisting of GBS 80, GBS 104 and GBS 322. Most preferably, the fusion peptide includes a polypeptide sequence from GBS 80. Accordingly, the invention includes a fusion peptide comprising a first amino acid sequence and a second amino acid sequence, wherein said first and second amino acid sequences are selected from a GBS antigen or a fragment thereof of the above antigen group. Preferably, the first and second amino acid sequences in the fusion polypeptide comprise different epitopes.

Example 7

Examples of Fragments for Fusion Proteins from GBS 80 with GBS 104, and GBS 322

Examples of GBS fragments for fusion proteins are provided from GBS 322, GBS 104, and GBS 80. One example of a fragment of GBS 322 in a fusion protein is a 407 amino acid fragment with the signal peptide removed. Fragments of GBS 104 may also be incorporated in fusion proteins. An example of GBS 104 fragments includes an 830 amino acid fragment, a 359 amino acid fragment from near the N-terminus, a 581 amino acid fragment from near the N-terminus, and a 740 amino acid fragment from near the N-terminus. Examples of GBS 80 fragments include a 446 amino acid fragment and a 235 amino acid fragment. Table 13 below summarizes the examples of fragments for fusion proteins and their locations within the corresponding full length GBS protein.

TABLE 13

Active Maternal Immunization Assay using combinations of GBS 80 with GBS 104 and GBS 322			
GBS	Size (AA)	SEQ ID NO	From . . . to
322	407	92	25-432
104	830	96	28-858
104 N1	359	97	28-387
104 N2	581	98	28-609
104 N3	740	99	28-768
80	446	100	37-483
80N	235	101	37-272

Hybrids (or fusions) consisting of amino acid sequences from two, three, four, five, six, seven, eight, nine, or ten GBS antigens are preferred. In particular, hybrids consisting of amino acid sequences from two, three, four, or five GBS antigens are preferred.

Different hybrid polypeptides may be mixed together in a single formulation. Within such combinations, a GBS antigen may be present in more than one hybrid polypeptide and/or as a non-hybrid polypeptide. It is preferred, however, that an antigen is present either as a hybrid or as a non-hybrid, but not as both.

Hybrid polypeptides can be represented by the formula $\text{NH}_2\text{-A-}\{ \text{-X-L-} \}_n\text{-B-COOH}$, wherein: X is an amino acid sequence of a GBS antigen or a fragment thereof from the antigen group set forth above; L is an optional linker amino acid sequence; A is an optional N-terminal amino acid sequence; B is an optional C-terminal amino acid sequence; and n is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

If a -X- moiety has a leader peptide sequence in its wild-type form, this may be included or omitted in the hybrid protein. In some embodiments, the leader peptides will be deleted except for that of the -X- moiety located at the N-terminus of the hybrid protein i.e. the leader peptide of X_1 will be retained, but the leader peptides of $X_2 \dots X_n$ will be omitted. This is equivalent to deleting all leader peptides and using the leader peptide of X_1 as moiety -A-.

For each n instances of $\{ \text{-X-L-} \}$, linker amino acid sequence -L- may be present or absent. For instance, when n=2 the hybrid may be $\text{NH}_2\text{X}_1\text{-L}_1\text{-X}_2\text{-L}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-X}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-L}_1\text{-X}_2\text{-COOH}$, $\text{NH}_2\text{-X}_1\text{-X}_2\text{-L}_2\text{-COOH}$, etc. Linker amino acid sequence(s)-L- will typically be short (e.g. 20 or fewer amino acids i.e. 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples comprise short peptide sequences which facilitate cloning, poly-glycine linkers (i.e. comprising Gly_n where n=2, 3, 4, 5, 6, 7, 8, 9, 10 or more), and histidine tags (i.e. His_n where n=3, 4, 5, 6, 7, 8, 9, 10 or more). Other suitable linker amino acid

sequences will be apparent to those skilled in the art. If X_1 lacks its own N-terminus methionine, -A- is preferably an oligopeptide (e.g. with 1, 2, 3, 4, 5, 6, 7 or 8 amino acids) which provides a N-terminus methionine.

-B- is an optional C-terminal amino acid sequence. This will typically be short (e.g. 40 or fewer amino acids i.e. 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include sequences to direct protein trafficking, short peptide sequences which facilitate cloning or purification (e.g. comprising histidine tags i.e. His_n where n=3, 4, 5, 6, 7, 8, 9, 10 or more), or sequences which enhance protein stability. Other suitable C-terminal amino acid sequences will be apparent to those skilled in the art. Most preferably, n is 2 or 3.

Example 8

Active Maternal Immunization Assay using fusion proteins of Fragments of GBS 80, GBS 67, and GBS 322

In this example, fusion proteins of GBS antigens was used in the Active Maternal Immunization Assay with an isolate challenge of different GBS strains. In these experiments, the challenge dose for the different GBS strains was sufficient to kill approximately 70-90% of unimmunized pups and is equal to 10xLD 50% (where LD 50% is the statistically derived Median Lethal Dose). The maternal mice were immunized according to the Active Maternal Immunization Assay schedule described above with the fusion proteins of a GBS 80 antigen with GBS 322 antigen in the GBS strains set forth in Table 14 below. Survival % was observed with the GBS fusion proteins. As shown in Table 14, in this particular challenge study, the survival rates for the fusion proteins in all of the GBS strains achieved up to 79%.

TABLE 14

Active Maternal Immunization Assay using fusion proteins of GBS 80 with GBS 322											
GBS	COH1 (III)		CJB111 (V)		515 (Ia)		DK21 (II)		2603 (V)		
	Dead/ treated	Survival %	Dead/ treated	Survival %	Dead/ treated	Survival %	Dead/ treated	Survival %	Dead/ treated	Survival %	
80N-322	16/40	60	8/39	79	12/28	57	7/19	63	8/37	78	
80	4/24	83									
PBS	35/40	12	27/35	23	32/39	18	31/40	22	33/40	17	
80-322	12/27	55							12/38	68	
80	0/33	100	28/40	30							
322									1/16	94	
PBS	19/20	5	38/39	2	25/29	14			19/26	27	

sequences will be apparent to those skilled in the art. A useful linker is GSGGGG (SEQ ID NO:92), with the Gly-Ser dipeptide being formed from a BamHI restriction site, thus aiding cloning and manipulation, and the (Gly)₄ tetrapeptide being a typical poly-glycine linker.

-A- is an optional N-terminal amino acid sequence. This will typically be short (e.g. 40 or fewer amino acids i.e. 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include leader sequences to direct protein trafficking, or short peptide sequences which facilitate cloning or purification (e.g. histidine tags i.e. His_n where n=3, 4, 5, 6, 7, 8, 9, 10 or more). Other suitable N-terminal amino acid

Nucleic Acids

The invention also provides nucleic acid encoding the GBS antigens and/or the hybrid fusion polypeptides of the invention. Furthermore, the invention provides nucleic acid which can hybridise to these nucleic acids, preferably under "high stringency" conditions (e.g. 65° C. in a 0.1xSSC, 0.5% SDS solution).

Polypeptides of the invention can be prepared by various means (e.g. recombinant expression, purification from cell culture, chemical synthesis, etc.) and in various forms (e.g. native, fusions, non-glycosylated, lipidated, etc.). They are preferably prepared in substantially pure form (i.e. substantially free from other GAS or host cell proteins).

Nucleic acid according to the invention can be prepared in many ways (e.g. by chemical synthesis, from genomic or cDNA libraries, from the organism itself, etc.) and can take various forms (e.g. single stranded, double stranded, vectors, probes, etc.). They are preferably prepared in substantially pure form (ie. substantially free from other GBS or host cell nucleic acids).

The term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones (e.g. phosphorothioates, etc.), and also peptide nucleic acids (PNA), etc. The invention includes nucleic acid comprising sequences complementary to those described above (e.g. for antisense or probing purposes).

The invention also provides a process for producing a polypeptide of the invention, comprising the step of culturing a host cell transformed with nucleic acid of the invention under conditions which induce polypeptide expression.

The invention provides a process for producing a polypeptide of the invention, comprising the step of synthesising at least part of the polypeptide by chemical means.

The invention provides a process for producing nucleic acid of the invention, comprising the step of amplifying nucleic acid using a primer-based amplification method (e.g. PCR).

The invention provides a process for producing nucleic acid of the invention, comprising the step of synthesising at least part of the nucleic acid by chemical means.

Purification and Recombinant Expression

The GBS antigens of the invention may be isolated from *Streptococcus agalactiae*, or they may be recombinantly produced, for instance, in a heterologous host. Preferably, the GBS antigens are prepared using a heterologous host. The heterologous host may be prokaryotic (e.g. a bacterium) or eukaryotic. It is preferably *E. coli*, but other suitable hosts include *Bacillus subtilis*, *Vibrio cholerae*, *Salmonella typhi*, *Salmonella typhimurium*, *Neisseria lactamica*, *Neisseria cinerea*, *Mycobacteria* (e.g. *M. tuberculosis*), yeasts, etc.

Recombinant production of polypeptides is facilitated by adding a tag protein to the GBS antigen to be expressed as a fusion protein comprising the tag protein and the GBS antigen. Such tag proteins can facilitate purification, detection and stability of the expressed protein. Tag proteins suitable for use in the invention include a polyarginine tag (Arg-tag), polyhistidine tag (His-tag), FLAG-tag, Strep-tag, c-myc-tag, S-tag, calmodulin-binding peptide, cellulose-binding domain, SBP-tag, chitin-binding domain, glutathione S-transferase-tag (GST), maltose-binding protein, transcription termination anti-terminiation factor (NusA), *E. coli* thioredoxin (TrxA) and protein disulfide isomerase I (DsbA). Preferred tag proteins include His-tag and GST. A full discussion on the use of tag proteins can be found at Ref. 3.

After purification, the tag proteins may optionally be removed from the expressed fusion protein, i.e., by specifically tailored enzymatic treatments known in the art. Commonly used proteases include enterokinase, tobacco etch virus (TEV), thrombin, and factor X_a .

GBS Polysaccharides

The compositions of the invention may be further improved by including GBS polysaccharides. Preferably, the GBS antigen and the saccharide each contribute to the immunological response in a recipient. The combination is particularly advantageous where the saccharide and polypeptide provide protection from different GBS serotypes.

The combined antigens may be present as a simple combination where separate saccharide and polypeptide antigens are administered together, or they may be present as a conju-

gated combination, where the saccharide and polypeptide antigens are covalently linked to each other.

Thus the invention provides an immunogenic composition comprising (i) one or more GBS polypeptide antigens and (ii) one or more GBS saccharide antigens. The polypeptide and the polysaccharide may advantageously be covalently linked to each other to form a conjugate.

Between them, the combined polypeptide and saccharide antigens preferably cover (or provide protection from) two or more GBS serotypes (e.g. 2, 3, 4, 5, 6, 7, 8 or more serotypes). The serotypes of the polypeptide and saccharide antigens may or may not overlap. For example, the polypeptide might protect against serogroup II or V, while the saccharide protects against either serogroups Ia, Ib, or III. Preferred combinations protect against the following groups of serotypes: (1) serotypes Ia and Ib, (2) serotypes Ia and II, (3) serotypes Ia and III, (4) serotypes Ia and IV, (5) serotypes Ia and V, (6) serotypes Ia and VI, (7) serotypes Ia and VII, (8) serotypes Ia and VIII, (9) serotypes Ib and II, (10) serotypes Ib and III, (11) serotypes Ib and IV, (12) serotypes Ib and V, (13) serotypes Ib and VI, (14) serotypes Ib and VII, (15) serotypes Ib and VIII, (16) serotypes II and III, (17) serotypes II and IV, (18) serotypes II and V, (19) serotypes II and VI, (20) serotypes II and VII, (21) serotypes II and VIII, (22) serotypes III and IV, (23) serotypes III and V, (24) serotypes III and VI, (25) serotypes III and VII, (26) serotypes III and VIII, (27) serotypes IV and V, (28) serotypes IV and VI, (29) serotypes IV and VII, (30) serotypes IV and VIII, (31) serotypes V and VI, (32) serotypes V and VII, (33) serotypes V and VIII, (34) serotypes VI and VII, (35) serotypes VI and VIII, and (36) serotypes VII and VIII.

Still more preferably, the combinations protect against the following groups of serotypes: (1) serotypes Ia and II, (2) serotypes Ia and V, (3) serotypes Ib and II, (4) serotypes Ib and V, (5) serotypes III and II, and (6) serotypes III and V. Most preferably, the combinations protect against serotypes III and V.

Protection against serotypes II and V is preferably provided by polypeptide antigens. Protection against serotypes Ia, Ib and/or III may be polypeptide or saccharide antigens.

In one embodiment, the immunogenic composition comprises a GBS saccharide antigen and at least two GBS polypeptide antigens or fragments thereof, wherein said GBS saccharide antigen comprises a saccharide selected from GBS serotype Ia, Ib, and III, and wherein said GBS polypeptide antigens comprise a combination of at least two polypeptide or a fragment thereof selected from the antigen group consisting of GBS 80, GBS 91, GBS 104, GBS 184, GBS 276, GBS 305, GBS 322, GBS 330, GBS 338, GBS 361, GBS 404, GBS 690, and GBS 691. Preferably, the combination includes one or more of GBS 80, GBS 104 and GBS 322. Still more preferably, the combination includes GBS 80 or a fragment thereof.

In certain embodiments, the compositions of the invention do not include a GBS polysaccharide. In certain embodiments, the combination does not include one or more of the GBS antigens selected from the group consisting of GBS 4, GBS 22, GBS 85, GBS 338 and GBS 361.

Immunogenic Compositions and Medicaments

Compositions of the invention are preferably immunogenic compositions, and are more preferably vaccine compositions. The pH of the composition is preferably between 6 and 8, preferably about 7. The pH may be maintained by the use of a buffer. The composition may be sterile and/or pyrogen-free. The composition may be isotonic with respect to humans.

Vaccines according to the invention may either be prophylactic (i.e. to prevent infection) or therapeutic (i.e. to treat infection), but will typically be prophylactic. Accordingly, the invention includes a method for the therapeutic or prophylactic treatment of a *Streptococcus agalactiae* infection in an animal susceptible to streptococcal infection comprising administering to said animal a therapeutic or prophylactic amount of the immunogenic compositions of the invention.

The invention also provides a composition of the invention for use as a medicament. The medicament is preferably able to raise an immune response in a mammal (i.e. it is an immunogenic composition) and is more preferably a vaccine.

The invention also provides the use of the compositions of the invention in the manufacture of a medicament for raising an immune response in a mammal. The medicament is preferably a vaccine.

The invention also provides for a kit comprising a first component comprising a combination of GBS antigens.

The invention also provides a delivery device pre-filled with the immunogenic compositions of the invention.

The invention also provides a method for raising an immune response in a mammal comprising the step of administering an effective amount of a composition of the invention. The immune response is preferably protective and preferably involves antibodies and/or cell-mediated immunity. The method may raise a booster response.

The mammal is preferably a human. Where the vaccine is for prophylactic use, the human is preferably a female (either of child bearing age or a teenager). Alternatively, the human may be elderly (e.g., over the age of 50, 55, 60, 65, 70 or 75) and may have an underlying disease such as diabetes or cancer. Where the vaccine is for therapeutic use, the human is preferably a pregnant female or an elderly adult.

These uses and methods are preferably for the prevention and/or treatment of a disease caused by *Streptococcus agalactiae*. The compositions may also be effective against other streptococcal bacteria.

One way of checking efficacy of therapeutic treatment involves monitoring GBS infection after administration of the composition of the invention. One way of checking efficacy of prophylactic treatment involves monitoring immune responses against the GBS antigens in the compositions of the invention after administration of the composition.

Compositions of the invention will generally be administered directly to a patient. Direct delivery may be accomplished by parenteral injection (e.g. subcutaneously, intraperitoneally, intradermally, intravenously, intramuscularly, or to the interstitial space of a tissue), or by rectal, oral (e.g. tablet, spray), vaginal, topical, transdermal {e.g. see ref. 4} or transcutaneous {e.g. see refs. 5 & 6}, intranasal {e.g. see ref. 7}, ocular, aural, pulmonary or other mucosal administration.

The invention may be used to elicit systemic and/or mucosal immunity.

Dosage treatment can be a single dose schedule or a multiple dose schedule. Multiple doses may be used in a primary immunisation schedule and/or in a booster immunisation schedule. In a multiple dose schedule the various doses may be given by the same or different routes e.g. a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, etc.

The compositions of the invention may be prepared in various forms. For example, the compositions may be prepared as injectables, either as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared (e.g. a lyophilised composition). The composition may be prepared for topical administration e.g. as an ointment, cream or powder. The composition may be prepared for oral administration e.g.

as a tablet or capsule, as a spray, or as a syrup (optionally flavoured). The composition may be prepared for pulmonary administration e.g. as an inhaler, using a fine powder or a spray. The composition may be prepared as a suppository or pessary. The composition may be prepared for nasal, aural or ocular administration e.g. as drops. The composition may be in kit form, designed such that a combined composition is reconstituted just prior to administration to a patient. Such kits may comprise one or more antigens in liquid form and one or more lyophilised antigens.

Immunogenic compositions used as vaccines comprise an immunologically effective amount of antigen(s), as well as any other components, as needed. By 'immunologically effective amount', it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, age, the taxonomic group of individual to be treated (e.g. non-human primate, primate, etc.), the capacity of the individual's immune system to synthesise antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Further Components of the Composition

The composition of the invention will typically, in addition to the components mentioned above, comprise one or more 'pharmaceutically acceptable carriers', which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolised macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and lipid aggregates (such as oil droplets or liposomes). Such carriers are well known to those of ordinary skill in the art. The vaccines may also contain diluents, such as water, saline, glycerol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present. A thorough discussion of pharmaceutically acceptable excipients is available in reference 8.

Vaccines of the invention may be administered in conjunction with other immunoregulatory agents. In particular, compositions will usually include an adjuvant.

Preferred further adjuvants include, but are not limited to, one or more of the following set forth below:

A. Mineral Containing Compositions

Mineral containing compositions suitable for use as adjuvants in the invention include mineral salts, such as aluminium salts and calcium salts. The invention includes mineral salts such as hydroxides (e.g. oxyhydroxides), phosphates (e.g. hydroxyphosphates, orthophosphates), sulphates, etc. {e.g. see chapters 8 & 9 of ref. 9}, or mixtures of different mineral compounds, with the compounds taking any suitable form (e.g. gel, crystalline, amorphous, etc.), and with adsorption being preferred. The mineral containing compositions may also be formulated as a particle of metal salt. See ref. 10.

B. Oil-Emulsions

Oil-emulsion compositions suitable for use as adjuvants in the invention include squalene-water emulsions, such as MF59® (5% Squalene, 0.5% TWEEN® 80, and 0.5% SPAN® 85, formulated into submicron particles using a microfluidizer). See WO90/14837. See also, Frey et al., "Comparison of the safety, tolerability, and immunogenicity

of a MF59®-adjuvanted influenza vaccine and a non-adjuvanted influenza vaccine in non-elderly adults”, *Vaccine* (2003) 21:4234-4237.

Particularly preferred adjuvants for use in the compositions are submicron oil-in water emulsions. Preferred submicron oil-in-water emulsions for use herein are squalene/water emulsions optionally containing varying amounts of MFP-PE, such as a submicron oil-in-water emulsion containing 4-5% w/v squalene, 0.25-1.0% w/v TWEEN® 80 (polyoxyethylenesorbitan monooleate), and/or 0.25-1.0% SPAN® 85 (sorbitan trioleate), and, optionally, N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), for example, the submicron oil-in-water emulsion known as “MF59®” (International Publication No. WO 90/14837; U.S. Pat. Nos. 6,299,884 and 6,451,325, incorporated herein by reference in their entireties; and Ott et al., “MF59—Design and Evaluation of a Safe and Potent Adjuvant for Human Vaccines” in *Vaccine Design: The Subunit and Adjuvant Approach* (Powell, M. F. and Newman, M. J. eds.) Plenum Press, New York, 1995, pp. 277-296). MF59® contains 4-5% w/v Squalene (e.g., 4.3%), 0.25-0.5% w/v TWEEN® 80, and 0.5% w/v SPAN® 85 and optionally contains various amounts of MTP-PE, formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, Mass.). For example, MRP-PE may be present in an amount of about 0-500 µg/dose, more preferably 0-250 µg/dose and most preferably, 0-100 µg/dose. As used herein, the term “MF59-0” refers to the above submicron oil-in-water emulsion lacking MTP-PE, while the term MF59-MTP denotes a formulation that contains MTP-PE. For instance, “MF59® MF59 100” contains 100 µg MTP-PE per dose, and so on. MF69, another submicron oil-in-water emulsion for use herein, contains 4.3% w/v squalene, 0.25% w/v TWEEN® 80, and 0.75% w/v SPAN® 85 and optionally MRP-PE. Yet another submicron oil-in-water emulsion is MF75, also known as SAF, containing 10% squalene, 0.4% TWEEN® 80, 5% PLURONIC®-blocked polymer L121, and thr-MDP, also microfluidized into a submicron emulsion. MF75-MTP denotes an MF75 formulation that includes MTP, such as from 100-400 µg MTP-PE per dose.

Submicron oil-in-water emulsions, methods of making the same and immunostimulating agents, such as muramyl peptides, for use in the compositions, are described in detail in International Publication No. WO 90114837 and U.S. Pat. Nos. 6,299,884 and 6,451,325, incorporated herein by reference in their entireties.

Complete Freund's adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used as adjuvants in the invention.

C. Saponin Formulations

Saponin formulations, may also be used as adjuvants in the invention. Saponins are a heterogeneous group of sterol glycosides and triterpenoid glycosides that are found in the bark, leaves, stems, roots and even flowers of a wide range of plant species. Saponin from the bark of the *Quillaja saponaria* Molina tree have been widely studied as adjuvants. Saponin can also be commercially obtained from *Smilax ornata* (sarsapilla), *Gypsophilla paniculata* (brides veil), and *Saponaria officinalis* (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs.

Saponin compositions have been purified using High Performance Thin Layer Chromatography (HP-LC) and Reversed Phase High Performance Liquid Chromatography (RP-HPLC). Specific purified fractions using these tech-

niques have been identified, including QS7, QS17, QS18, QS21, QH-A, QH-B and QH-C. Preferably, the saponin QS21. A method of production of QS21 is disclosed in U.S. Pat. No. 5,057,540. Saponin formulations may also comprise a sterol, such as cholesterol (see WO 96/33739).

Combinations of saponins and cholesterol can be used to form unique particles called Immunostimulating Complexes (ISCOMs). ISCOMs typically also include a phospholipid such as phosphatidylethanolamine or phosphatidylcholine. Any known saponin can be used in ISCOMs. Preferably, the ISCOM includes one or more of Quil A, QHA and QHC. ISCOMs are further described in EP 0 109 942, WO 96/11711 and WO 96/33739. Optionally, the ISCOMS may be devoid of additional detergent. See ref. 11.

A review of the development of saponin based adjuvants can be found at ref. 12.

C. Virosomes and Virus Like Particles (VLPs)

Virosomes and Virus Like Particles (VLPs) can also be used as adjuvants in the invention. These structures generally contain one or more proteins from a virus optionally combined or formulated with a phospholipid. They are generally non-pathogenic, non-replicating and generally do not contain any of the native viral genome. The viral proteins may be recombinantly produced or isolated from whole viruses. These viral proteins suitable for use in virosomes or VLPs include proteins derived from influenza virus (such as HA or NA), Hepatitis B virus (such as core or capsid proteins), Hepatitis E virus, measles virus, Sindbis virus, Rotavirus, Foot-and-Mouth Disease virus, Retrovirus, Norwalk virus, human Papilloma virus, HUV, RNA-phages, QB-phage (such as coat proteins), GA-phage, fr-phage, AP205 phage, and Ty (such as retrotransposon Ty protein p1). VLPs are discussed further in WO 03/024480, WO 03/024481, and Refs. 13, 14, 15 and 16. Virosomes are discussed further in, for example, Ref. 17.

D. Bacterial or Microbial Derivatives

Adjuvants suitable for use in the invention include bacterial or microbial derivatives such as:

(1) Non-Toxic Derivatives of Enterobacterial Lipopolysaccharide (LPS)

Such derivatives include Monophosphoryl lipid A (MPL) and 3-O-deacylated MPL (3dMPL). 3dMPL is a mixture of 3 De-O-acylated monophosphoryl lipid A with 4, 5 or 6 acylated chains. A preferred “small particle” form of 3 De-O-acylated monophosphoryl lipid A is disclosed in EP 0 689 454. Such “small particles” of 3dMPL are small enough to be sterile filtered through a 0.22 micron membrane (see EP 0 689 454). Other non-toxic LPS derivatives include monophosphoryl lipid A mimics, such as aminoalkyl glucosaminide phosphate derivatives e.g. RC-529. See Ref. 18.

(2) Lipid A Derivatives

Lipid A derivatives include derivatives of lipid A from *Escherichia coli* such as OM-174. OM-174 is described for example in Ref. 19 and 20.

(3) Immunostimulatory Oligonucleotides

Immunostimulatory oligonucleotides suitable for use as adjuvants in the invention include nucleotide sequences containing a CpG motif (a sequence containing an unmethylated cytosine followed by guanosine and linked by a phosphate bond). Bacterial double stranded RNA or oligonucleotides containing palindromic or poly(dG) sequences have also been shown to be immunostimulatory.

The CpG's can include nucleotide modifications/analogs such as phosphorothioate modifications and can be double-stranded or single-stranded. Optionally, the guanosine may be replaced with an analog such as 2'-deoxy-7-deazaguanosine. See ref. 21, WO 02/26757 and WO 99/62923 for

examples of possible analog substitutions. The adjuvant effect of CpG oligonucleotides is further discussed in Refs. 22, 23, WO 98/40100, U.S. Pat. No. 6,207,646, U.S. Pat. No. 6,239,116, and U.S. Pat. No. 6,429,199.

The CpG sequence may be directed to TLR9, such as the motif GTCGTT or TTCGTT. See ref. 24. The CpG sequence may be specific for inducing a Th1 immune response, such as a CpG-A ODN, or it may be more specific for inducing a B cell response, such as a CpG-B ODN. CpG-A and CpG-B ODNs are discussed in refs. 25, 26 and WO 01/95935. Preferably, the CpG is a CpG-A ODN.

Preferably, the CpG oligonucleotide is constructed so that the 5' end is accessible for receptor recognition. Optionally, two CpG oligonucleotide sequences may be attached at their 3' ends to form "immunomers". See, for example, refs. 27, 28, 29 and WO 03/035836.

(4) ADP-Ribosylating Toxins and Detoxified Derivatives Thereof.

Bacterial ADP-ribosylating toxins and detoxified derivatives thereof may be used as adjuvants in the invention. Preferably, the protein is derived from *E. coli* (i.e., *E. coli* heat labile enterotoxin "LT", cholera ("CT"), or pertussis ("PT")). The use of detoxified ADP-ribosylating toxins as mucosal adjuvants is described in WO 95/17211 and as parenteral adjuvants in WO 98/42375. Preferably, the adjuvant is a detoxified LT mutant such as LT-K63.

E. Human Immunomodulators

Human immunomodulators suitable for use as adjuvants in the invention include cytokines, such as interleukins (e.g. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g. interferon- γ), macrophage colony stimulating factor, and tumor necrosis factor.

F. Bioadhesives and Mucoadhesives

Bioadhesives and mucoadhesives may also be used as adjuvants in the invention. Suitable bioadhesives include esterified hyaluronic acid microspheres (Ref. 30) or mucoadhesives such as cross-linked derivatives of poly(acrylic acid), polyvinyl alcohol, polyvinyl pyrrolidone, polysaccharides and carboxymethylcellulose. Chitosan and derivatives thereof may also be used as adjuvants in the invention. E.g., ref. 31.

G. Microparticles

Microparticles may also be used as adjuvants in the invention. Microparticles (i.e. a particle of ~100 nm to ~150 μ m in diameter, more preferably 200 nm to ~30 μ m in diameter, and most preferably ~500-nm to ~10 μ m in diameter) formed from materials that are biodegradable and non-toxic (e.g. a poly(α -hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone, etc.), with poly(lactide-co-glycolide) are preferred, optionally treated to have a negatively-charged surface (e.g. with SDS) or a positively-charged surface (e.g. with a cationic detergent, such as CTAB).

H. Liposomes

Examples of liposome formulations suitable for use as adjuvants are described in U.S. Pat. No. 6,090,406, U.S. Pat. No. 5,916,588, and EP 0 626 169.

I. Polyoxyethylene ether and Polyoxyethylene Ester Formulations

Adjuvants suitable for use in the invention include polyoxyethylene ethers and polyoxyethylene esters. Ref. 32. Such formulations further include polyoxyethylene sorbitan ester surfactants in combination with an octoxynol (Ref. 33) as well as polyoxyethylene alkyl ethers or ester surfactants in combination with at least one additional non-ionic surfactant such as an octoxynol (Ref. 34).

Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether (laureth 9), polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.

J. Polyphosphazene (PCPP)

PCPP formulations are described, for example, in Ref. 35 and 36.

K. Muramyl Peptides

Examples of muramyl peptides suitable for use as adjuvants in the invention include N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), and N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine MTP-PE).

L. Imidazoquinolone Compounds

Examples of imidazoquinolone compounds suitable for use as adjuvants in the invention include Imiquimod and its homologues, described further in Ref 37 and 38.

The invention may also comprise combinations of aspects of one or more of the adjuvants identified above. For example, the following adjuvant compositions may be used in the invention:

- (1) a saponin and an oil-in-water emulsion (ref. 39);
 - (2) a saponin (e.g., QS21)+a non-toxic LPS derivative (e.g., 3dMPL) (see WO 94/00153);
 - (3) a saponin (e.g., QS21)+a non-toxic LPS derivative (e.g., 3dMPL)+a cholesterol;
 - (4) a saponin (e.g. QS21)+3dMPL+IL-12 (optionally+a sterol) (Ref. 40);
 - (5) combinations of 3dMPL with, for example, QS21 and/or oil-in-water emulsions (Ref. 41);
 - (6) SAF, containing 10% Squalane, 0.4% TWEEN® 80, 5% PLURONIC®-block polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion.
 - (7) RIBI™ adjuvant system (RAS), (Ribi Immunochem) containing 2% Squalene, 0.2% TWEEN® 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL+CWS (DETOX™); and
 - (8) one or more mineral salts (such as an aluminum salt)+a non-toxic derivative of LPS (such as 3dPML).
- Aluminium salts and MF59 are preferred adjuvants for parenteral immunisation. Mutant bacterial toxins are preferred mucosal adjuvants.

The composition may include an antibiotic.

Further Antigens

The compositions of the invention may further comprise one or more additional non-GBS antigens, including additional bacterial, viral or parasitic antigens.

In another embodiment, the GBS antigen combinations of the invention are combined with one or more additional, non-GBS antigens suitable for use in a vaccine designed to protect elderly or immunocompromised individuals. For example, the GBS antigen combinations may be combined with an antigen derived from the group consisting of *Enterococcus faecalis*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Pseudomonas aeruginosa*, *Legionella pneumophila*, *Listeria monocytogenes*, *Neisseria meningitidis*, influenza, and Parainfluenza virus ('PIV').

Where a saccharide or carbohydrate antigen is used, it is preferably conjugated to a carrier protein in order to enhance immunogenicity {e.g. refs. 42 to 51}. Preferred carrier proteins are bacterial toxins or toxoids, such as diphtheria or tetanus toxoids. The CRM₁₉₇ diphtheria toxoid is particularly

preferred {52}. Other carrier polypeptides include the *N. meningitidis* outer membrane protein {53}, synthetic peptides {54, 55}, heat shock proteins {56, 57}, pertussis proteins {58, 59}, protein D from *H. influenzae* {60}, cytokines {61}, lymphokines, hormones, growth factors, toxin A or B from *C. difficile* {62}, iron-uptake proteins {63}, etc. Where a mixture comprises capsular saccharides from both serogroups A and C, it may be preferred that the ratio (w/w) of MenA saccharide:MenC saccharide is greater than 1 (e.g. 2:1, 3:1, 4:1, 5:1, 10:1 or higher). Different saccharides can be conjugated to the same or different type of carrier protein. Any suitable conjugation reaction can be used, with any suitable linker where necessary.

Toxic protein antigens may be detoxified where necessary e.g. detoxification of pertussis toxin by chemical and/or genetic means.

Where a diphtheria antigen is included in the composition it is preferred also to include tetanus antigen and pertussis antigens. Similarly, where a tetanus antigen is included it is preferred also to include diphtheria and pertussis antigens. Similarly, where a pertussis antigen is included it is preferred also to include diphtheria and tetanus antigens.

Antigens in the composition will typically be present at a concentration of at least 1 µg/ml each. In general, the concentration of any given antigen will be sufficient to elicit an immune response against that antigen.

As an alternative to using protein antigens in the composition of the invention, nucleic acid encoding the antigen may be used {e.g. refs. 64 to 72}. Protein components of the compositions of the invention may thus be replaced by nucleic acid (preferably DNA e.g. in the form of a plasmid) that encodes the protein.

DEFINITIONS

The term "comprising" means "including" as well as "consisting" e.g. a composition "comprising" X may consist exclusively of X or may include something additional e.g. X+Y.

The term "about" in relation to a numerical value x means, for example, $X \pm 10\%$.

References to a percentage sequence identity between two amino acid sequences means that, when aligned, that percentage of amino acids are the same in comparing the two sequences. This alignment and the percent homology or sequence identity can be determined using software programs known in the art, for example those described in section 7.7.18 of reference 73. A preferred alignment is determined by the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is disclosed in reference 74.

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SEQUENCE LISTING

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Lys	Ala	Val	Leu	Gly	Lys	Ala	Ile	Glu	Asn	Thr	Phe	Glu	Leu	Gln	Tyr
305					310					315					320
Asp	His	Thr	Pro	Asp	Lys	Ala	Asp	Asn	Pro	Lys	Pro	Ser	Asn	Pro	Pro
			325					330						335	
Arg	Lys	Pro	Glu	Val	His	Thr	Gly	Gly	Lys	Arg	Phe	Val	Lys	Lys	Asp
			340					345				350			
Ser	Thr	Glu	Thr	Gln	Thr	Leu	Gly	Gly	Ala	Glu	Phe	Asp	Leu	Leu	Ala
355							360					365			
Ser	Asp	Gly	Thr	Ala	Val	Lys	Trp	Thr	Asp	Ala	Leu	Ile	Lys	Ala	Asn
370						375					380				
Thr	Asn	Lys	Asn	Tyr	Ile	Al									

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450	455	460
Thr Val Asp Ser Ala	Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys	
465	470	475 480
Arg Pro Ser Ile	Pro Asn Thr Gly Gly Ile Gly Thr Ala Ile Phe Val	
	485 490 495	
Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val Lys Gly Met Lys Arg		
	500 505 510	
Arg Thr Lys Asp Asn		
515		
<210> SEQ ID NO 4		
<211> LENGTH: 525		
<212> TYPE: PRT		
<213> ORGANISM: Streptococcus agalactiae		
<400> SEQUENCE: 4		
Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met		
1 5 10 15		
Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met		
	20 25 30	
Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr		
	35 40 45	
Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile		
	50 55 60	
Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn		
65 70 75 80		
Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe		
	85 90 95	
Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys		
	100 105 110	
Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu		
	115 120 125	
Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val		
	130 135 140	
Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp		
145 150 155 160		
Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe		
	165 170 175	
Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser		
	180 185 190	
Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr		
	195 200 205	
Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile		
	210 215 220	
Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu		
225 230 235 240		
Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu		
	245 250 255	
Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn		
	260 265 270	
Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn		
	275 280 285	
Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu		
	290 295 300	

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Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
305                      310                      315                      320

Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
                      325                      330                      335

Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr
                      340                      345                      350

Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys
                      355                      360                      365

Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg
                      370                      375                      380

Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu
385                      390                      395                      400

Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala
                      405                      410                      415

Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val
                      420                      425                      430

Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu
435                      440                      445

Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala
450                      455                      460

Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile
465                      470                      475                      480

Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr
                      485                      490                      495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500                      505                      510

Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly
515                      520                      525

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<210> SEQ ID NO 5
<211> LENGTH: 5
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 5

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Ile Pro Asn Thr Gly
1          5

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<210> SEQ ID NO 6
<211> LENGTH: 520
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 6

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Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
1          5          10          15

Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
20          25          30

Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
35          40          45

Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
50          55          60

Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65          70          75          80

Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85          90          95

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Lys	Arg	Tyr	Lys	Val	Lys	Thr	Asp	Ile	Ser	Val	Asp	Glu	Leu	Lys	Lys	100	105	110	
Leu	Thr	Thr	Val	Glu	Ala	Ala	Asp	Ala	Lys	Val	Gly	Thr	Ile	Leu	Glu	115	120	125	
Glu	Gly	Val	Ser	Leu	Pro	Gln	Lys	Thr	Asn	Ala	Gln	Gly	Leu	Val	Val	130	135	140	
Asp	Ala	Leu	Asp	Ser	Lys	Ser	Asn	Val	Arg	Tyr	Leu	Tyr	Val	Glu	Asp	145	150	155	160
Leu	Lys	Asn	Ser	Pro	Ser	Asn	Ile	Thr	Lys	Ala	Tyr	Ala	Val	Pro	Phe	165	170	175	
Val	Leu	Glu	Leu	Pro	Val	Ala	Asn	Ser	Thr	Gly	Thr	Gly	Phe	Leu	Ser	180	185	190	
Glu	Ile	Asn	Ile	Tyr	Pro	Lys	Asn	Val	Val	Thr	Asp	Glu	Pro	Lys	Thr	195	200	205	
Asp	Lys	Asp	Val	Lys	Lys	Leu	Gly	Gln	Asp	Asp	Ala	Gly	Tyr	Thr	Ile	210	215	220	
Gly	Glu	Glu	Phe	Lys	Trp	Phe	Leu	Lys	Ser	Thr	Ile	Pro	Ala	Asn	Leu	225	230	235	240
Gly	Asp	Tyr	Glu	Lys	Phe	Glu	Ile	Thr	Asp	Lys	Phe	Ala	Asp	Gly	Leu	245	250	255	
Thr	Tyr	Lys	Ser	Val	Gly	Lys	Ile	Lys	Ile	Gly	Ser	Lys	Thr	Leu	Asn	260	265	270	
Arg	Asp	Glu	His	Tyr	Thr	Ile	Asp	Glu	Pro	Thr	Val	Asp	Asn	Gln	Asn	275	280	285	
Thr	Leu	Lys	Ile	Thr	Phe	Lys	Pro	Glu	Lys	Phe	Lys	Glu	Ile	Ala	Glu	290	295	300	
Leu	Leu	Lys	Gly	Met	Thr	Leu	Val	Lys	Asn	Gln	Asp	Ala	Leu	Asp	Lys	305	310	315	320
Ala	Thr	Ala	Asn	Thr	Asp	Asp	Ala	Ala	Phe	Leu	Glu	Ile	Pro	Val	Ala	325	330	335	
Ser	Thr	Ile	Asn	Glu	Lys	Ala	Val	Leu	Gly	Lys	Ala	Ile	Glu	Asn	Thr	340	345	350	
Phe	Glu	Leu	Gln	Tyr	Asp	His	Thr	Pro	Asp	Lys	Ala	Asp	Asn	Pro	Lys	355	360	365	
Pro	Ser	Asn	Pro	Pro	Arg	Lys	Pro	Glu	Val	His	Thr	Gly	Gly	Lys	Arg	370	375	380	
Phe	Val	Lys	Lys	Asp	Ser	Thr	Glu	Thr	Gln	Thr	Leu	Gly	Gly	Ala	Glu	385	390	395	400
Phe	Asp	Leu	Leu	Ala	Ser	Asp	Gly	Thr	Ala	Val	Lys	Trp	Thr	Asp	Ala	405	410	415	
Leu	Ile	Lys	Ala	Asn	Thr	Asn	Lys	Asn	Tyr	Ile	Ala	Gly	Glu	Ala	Val	420	425	430	
Thr	Gly	Gln	Pro	Ile	Lys	Leu	Lys	Ser	His	Thr	Asp	Gly	Thr	Phe	Glu	435	440	445	
Ile	Lys	Gly	Leu	Ala	Tyr	Ala	Val	Asp	Ala	Asn	Ala	Glu	Gly	Thr	Ala	450	455	460	
Val	Thr	Tyr	Lys	Leu	Lys	Glu	Thr	Lys	Ala	Pro	Glu	Gly	Tyr	Val	Ile	465	470	475	480
Pro	Asp	Lys	Glu	Ile	Glu	Phe	Thr	Val	Ser	Gln	Thr	Ser	Tyr	Asn	Thr	485	490	495	
Lys	Pro	Thr	Asp	Ile	Thr	Val	Asp	Ser	Ala	Asp	Ala	Thr	Pro	Asp	Thr	500	505	510	
Ile	Lys	Asn	Asn	Lys	Arg	Pro	Ser												

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515	520
<210> SEQ ID NO 7	
<211> LENGTH: 483	
<212> TYPE: PRT	
<213> ORGANISM: Streptococcus agalactiae	
<400> SEQUENCE: 7	
Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr	
1 5 10 15	
Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile Thr Ser Asn Gly Gly	
20 25 30	
Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly	
35 40 45	
Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val	
50 55 60	
Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu	
65 70 75 80	
Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu	
85 90 95	
Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val Asp Ala Leu Asp Ser	
100 105 110	
Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro	
115 120 125	
Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro	
130 135 140	
Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr	
145 150 155 160	
Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys	
165 170 175	
Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys	
180 185 190	
Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys	
195 200 205	
Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val	
210 215 220	
Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His Tyr	
225 230 235 240	
Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile Thr	
245 250 255	
Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly Met	
260 265 270	
Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys Ala Thr Ala Asn Thr	
275 280 285	
Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala Ser Thr Ile Asn Glu	
290 295 300	
Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr Phe Glu Leu Gln Tyr	
305 310 315 320	
Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys Pro Ser Asn Pro Pro	
325 330 335	
Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg Phe Val Lys Lys Asp	
340 345 350	
Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu Phe Asp Leu Leu Ala	
355 360 365	

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Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala Asn
 370 375 380
 Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val Thr Gly Gln Pro Ile
 385 390 395 400
 Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu Ile Lys Gly Leu Ala
 405 410 415
 Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala Val Thr Tyr Lys Leu
 420 425 430
 Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile Pro Asp Lys Glu Ile
 435 440 445
 Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr Lys Pro Thr Asp Ile
 450 455 460
 Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn Lys
 465 470 475 480
 Arg Pro Ser

<210> SEQ ID NO 8
 <211> LENGTH: 271
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 8

Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr Thr Val Asn Ile Tyr
 1 5 10 15
 Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile Thr Ser Asn Gly Gly
 20 25 30
 Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn Tyr Ala Lys Leu Gly
 35 40 45
 Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe Lys Arg Tyr Lys Val
 50 55 60
 Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys Leu Thr Thr Val Glu
 65 70 75 80
 Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu Glu Gly Val Ser Leu
 85 90 95
 Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val Asp Ala Leu Asp Ser
 100 105 110
 Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp Leu Lys Asn Ser Pro
 115 120 125
 Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe Val Leu Glu Leu Pro
 130 135 140
 Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser Glu Ile Asn Ile Tyr
 145 150 155 160
 Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr Asp Lys Asp Val Lys
 165 170 175
 Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile Gly Glu Glu Phe Lys
 180 185 190
 Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu Gly Asp Tyr Glu Lys
 195 200 205
 Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu Thr Tyr Lys Ser Val
 210 215 220
 Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn Arg Asp Glu His Tyr
 225 230 235 240
 Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn Thr Leu Lys Ile Thr
 245 250 255

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Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu Leu Leu Lys Gly
260 265 270

<210> SEQ ID NO 9
 <211> LENGTH: 212
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 9

Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys Ala Thr Ala Asn
1 5 10 15
 Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala Ser Thr Ile Asn
20 25 30
 Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr Phe Glu Leu Gln
35 40 45
 Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys Pro Ser Asn Pro
50 55 60
 Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg Phe Val Lys Lys
65 70 75 80
 Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu Phe Asp Leu Leu
85 90 95
 Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala Leu Ile Lys Ala
100 105 110
 Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val Thr Gly Gln Pro
115 120 125
 Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu Ile Lys Gly Leu
130 135 140
 Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala Val Thr Tyr Lys
145 150 155 160
 Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile Pro Asp Lys Glu
165 170 175
 Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr Lys Pro Thr Asp
180 185 190
 Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr Ile Lys Asn Asn
195 200 205
 Lys Arg Pro Ser
210

<210> SEQ ID NO 10
 <211> LENGTH: 1629
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 10

atgaaaaaag gacaagtaaa tgatactaag caatcttact ctctacgtaa atataaatTT 60
 ggtttagcat cagtaatTTT agggtcattc ataatggTca caagtcctgt ttttgcggtat 120
 caaactacat cggttcaagt taataatcag acaggcacta gtgtggatgc taataattct 180
 tccaatgaga caagtgcgc aagtgtgatt acttccaata atgatatgtt tcaagcgtct 240
 gataaagttg taaatagtca aaatacggca acaaaggaca ttactactcc tttagtagag 300
 acaaagccaa tggTggaaaa aacattacct gaacaaggga attatgttta tagcaaagaa 360
 accgaggtga aaaatacacc ttcaaaatca gccccagtag ctttctatgc aaagaaaggt 420
 gataaagttt tctatgacca agtatttTaat aaagataatg tgaatggat tTcatataag 480
 tctttttgtg gcgtacgtcg atacgcagct attgagtcac tagatccatc aggaggttca 540

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gagactaaag cacctactcc tgtaacaaat tcaggaagca ataatcaaga gaaaatagca 600
acgcaaggaa attatacatt ttcacataaa gtagaagtaa aaaatgaagc taaggtagcg 660
agtccaactc aatttacatt ggacaaagga gacagaatTT tttacgacca aatactaact 720
attgaaggaa atcagtgggt atcttataaa tcattcaatg gtgttcgtcg tttgttttg 780
ctaggtaaag catcttcagt agaaaaaact gaagataaag aaaagtgtc tcctcaacca 840
caagcccgta ttactaaaac tggtagactg actatttcta acgaaacaac tacaggTTTT 900
gatattttaa ttacgaatat taaagatgat aacggtatcg ctgctgttaa ggtaccggtt 960
tggactgaac aaggaggggc agatgatatt aaatgggata cagctgtaac tactggggat 1020
ggcaactaca aagtagctgt atcatttgct gaccataaga atgagaaggg tctttataat 1080
attcatttat actaccaaga agctagtggg acacttgtag gtgtaacagg aactaaagtg 1140
acagtagctg gaactaatc ttctcaagaa cctattgaaa atggtttagc aaagactggg 1200
gtttataata ttatcggaag tactgaagta aaaaatgaag ctaaaatatac aagtcagacc 1260
caatttactt tagaaaaagg tgacaaaata aattatgatc aagtattgac agcagatggg 1320
taccagtgga tttcttaca atcttatagt ggtgttcgtc gctatattcc tgtgaaaaag 1380
ctaactaca gtagtgaaaa agcgaaagat gaggcgacta aaccgactag ttatcccaac 1440
ttacctaaaa caggtagccta tacatttact aaaactgtag atgtgaaaag tcaacctaaa 1500
gtatcaagtc cagtgaatt taattttcaa aagggtgaaa aaatacatta tgatcaagtg 1560
ttagtagtag atggtcacat gtggatttca tacaagagtt attccgggat tcgtcgtat 1620
attgaaatt 1629

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<210> SEQ ID NO 11

<211> LENGTH: 543

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 11

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Met Lys Lys Gly Gln Val Asn Asp Thr Lys Gln Ser Tyr Ser Leu Arg
 1             5             10             15

Lys Tyr Lys Phe Gly Leu Ala Ser Val Ile Leu Gly Ser Phe Ile Met
          20             25             30

Val Thr Ser Pro Val Phe Ala Asp Gln Thr Thr Ser Val Gln Val Asn
          35             40             45

Asn Gln Thr Gly Thr Ser Val Asp Ala Asn Asn Ser Ser Asn Glu Thr
          50             55             60

Ser Ala Ser Ser Val Ile Thr Ser Asn Asn Asp Ser Val Gln Ala Ser
          65             70             75             80

Asp Lys Val Val Asn Ser Gln Asn Thr Ala Thr Lys Asp Ile Thr Thr
          85             90             95

Pro Leu Val Glu Thr Lys Pro Met Val Glu Lys Thr Leu Pro Glu Gln
          100            105            110

Gly Asn Tyr Val Tyr Ser Lys Glu Thr Glu Val Lys Asn Thr Pro Ser
          115            120            125

Lys Ser Ala Pro Val Ala Phe Tyr Ala Lys Lys Gly Asp Lys Val Phe
          130            135            140

Tyr Asp Gln Val Phe Asn Lys Asp Asn Val Lys Trp Ile Ser Tyr Lys
          145            150            155            160

Ser Phe Cys Gly Val Arg Arg Tyr Ala Ala Ile Glu Ser Leu Asp Pro
          165            170            175

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Ser Gly Gly Ser Glu Thr Lys Ala Pro Thr Pro Val Thr Asn Ser Gly
    180                      185                      190

Ser Asn Asn Gln Glu Lys Ile Ala Thr Gln Gly Asn Tyr Thr Phe Ser
    195                      200                      205

His Lys Val Glu Val Lys Asn Glu Ala Lys Val Ala Ser Pro Thr Gln
    210                      215                      220

Phe Thr Leu Asp Lys Gly Asp Arg Ile Phe Tyr Asp Gln Ile Leu Thr
    225                      230                      235                      240

Ile Glu Gly Asn Gln Trp Leu Ser Tyr Lys Ser Phe Asn Gly Val Arg
    245                      250                      255

Arg Phe Val Leu Leu Gly Lys Ala Ser Ser Val Glu Lys Thr Glu Asp
    260                      265                      270

Lys Glu Lys Val Ser Pro Gln Pro Gln Ala Arg Ile Thr Lys Thr Gly
    275                      280                      285

Arg Leu Thr Ile Ser Asn Glu Thr Thr Thr Gly Phe Asp Ile Leu Ile
    290                      295                      300

Thr Asn Ile Lys Asp Asp Asn Gly Ile Ala Ala Val Lys Val Pro Val
    305                      310                      315                      320

Trp Thr Glu Gln Gly Gly Gln Asp Asp Ile Lys Trp Tyr Thr Ala Val
    325                      330                      335

Thr Thr Gly Asp Gly Asn Tyr Lys Val Ala Val Ser Phe Ala Asp His
    340                      345                      350

Lys Asn Glu Lys Gly Leu Tyr Asn Ile His Leu Tyr Tyr Gln Glu Ala
    355                      360                      365

Ser Gly Thr Leu Val Gly Val Thr Gly Thr Lys Val Thr Val Ala Gly
    370                      375                      380

Thr Asn Ser Ser Gln Glu Pro Ile Glu Asn Gly Leu Ala Lys Thr Gly
    385                      390                      395                      400

Val Tyr Asn Ile Ile Gly Ser Thr Glu Val Lys Asn Glu Ala Lys Ile
    405                      410                      415

Ser Ser Gln Thr Gln Phe Thr Leu Glu Lys Gly Asp Lys Ile Asn Tyr
    420                      425                      430

Asp Gln Val Leu Thr Ala Asp Gly Tyr Gln Trp Ile Ser Tyr Lys Ser
    435                      440                      445

Tyr Ser Gly Val Arg Arg Tyr Ile Pro Val Lys Lys Leu Thr Thr Ser
    450                      455                      460

Ser Glu Lys Ala Lys Asp Glu Ala Thr Lys Pro Thr Ser Tyr Pro Asn
    465                      470                      475                      480

Leu Pro Lys Thr Gly Thr Tyr Thr Phe Thr Lys Thr Val Asp Val Lys
    485                      490                      495

Ser Gln Pro Lys Val Ser Ser Pro Val Glu Phe Asn Phe Gln Lys Gly
    500                      505                      510

Glu Lys Ile His Tyr Asp Gln Val Leu Val Val Asp Gly His Gln Trp
    515                      520                      525

Ile Ser Tyr Lys Ser Tyr Ser Gly Ile Arg Arg Tyr Ile Glu Ile
    530                      535                      540

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<210> SEQ ID NO 12

<211> LENGTH: 504

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 12

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Asp Gln Thr Thr Ser Val Gln Val Asn Asn Gln Thr Gly Thr Ser Val
  1              5              10              15

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Asp	Ala	Asn	Asn	Ser	Ser	Asn	Glu	Thr	Ser	Ala	Ser	Ser	Val	Ile	Thr
		20						25					30		
Ser	Asn	Asn	Asp	Ser	Val	Gln	Ala	Ser	Asp	Lys	Val	Val	Asn	Ser	Gln
		35					40					45			
Asn	Thr	Ala	Thr	Lys	Asp	Ile	Thr	Thr	Pro	Leu	Val	Glu	Thr	Lys	Pro
50						55				60					
Met	Val	Glu	Lys	Thr	Leu	Pro	Glu	Gln	Gly	Asn	Tyr	Val	Tyr	Ser	Lys
65					70					75					80
Glu	Thr	Glu	Val	Lys	Asn	Thr	Pro	Ser	Lys	Ser	Ala	Pro	Val	Ala	Phe
				85					90					95	
Tyr	Ala	Lys	Lys	Gly	Asp	Lys	Val	Phe	Tyr	Asp	Gln	Val	Phe	Asn	Lys
		100						105					110		
Asp	Asn	Val	Lys	Trp	Ile	Ser	Tyr	Lys	Ser	Phe	Cys	Gly	Val	Arg	Arg
		115					120					125			
Tyr	Ala	Ala	Ile	Glu	Ser	Leu	Asp	Pro	Ser	Gly	Gly	Ser	Glu	Thr	Lys
130						135					140				
Ala	Pro	Thr	Pro	Val	Thr	Asn	Ser	Gly	Ser	Asn	Asn	Gln	Glu	Lys	Ile
145					150					155					160
Ala	Thr	Gln	Gly	Asn	Tyr	Thr	Phe	Ser	His	Lys	Val	Glu	Val	Lys	Asn
				165					170					175	
Glu	Ala	Lys	Val	Ala	Ser	Pro	Thr	Gln	Phe	Thr	Leu	Asp	Lys	Gly	Asp
		180						185					190		
Arg	Ile	Phe	Tyr	Asp	Gln	Ile	Leu	Thr	Ile	Glu	Gly	Asn	Gln	Trp	Leu
		195					200					205			
Ser	Tyr	Lys	Ser	Phe	Asn	Gly	Val	Arg	Arg	Phe	Val	Leu	Leu	Gly	Lys
210						215					220				
Ala	Ser	Ser	Val	Glu	Lys	Thr	Glu	Asp	Lys	Glu	Lys	Val	Ser	Pro	Gln
225					230					235					240
Pro	Gln	Ala	Arg	Ile	Thr	Lys	Thr	Gly	Arg	Leu	Thr	Ile	Ser	Asn	Glu
				245					250					255	
Thr	Thr	Thr	Gly	Phe	Asp	Ile	Leu	Ile	Thr	Asn	Ile	Lys	Asp	Asp	Asn
		260						265					270		
Gly	Ile	Ala	Ala	Val	Lys	Val	Pro	Val	Trp	Thr	Glu	Gln	Gly	Gly	Gln
		275					280					285			
Asp	Asp	Ile	Lys	Trp	Tyr	Thr	Ala	Val	Thr	Thr	Gly	Asp	Gly	Asn	Tyr
290						295					300				
Lys	Val	Ala	Val	Ser	Phe	Ala	Asp	His	Lys	Asn	Glu	Lys	Gly	Leu	Tyr
305					310					315					320
Asn	Ile	His	Leu	Tyr	Tyr	Gln	Glu	Ala	Ser	Gly	Thr	Leu	Val	Gly	Val
			325						330					335	
Thr	Gly	Thr	Lys	Val	Thr	Val	Ala	Gly	Thr	Asn	Ser	Ser	Gln	Glu	Pro
		340						345					350		
Ile	Glu	Asn	Gly	Leu	Ala	Lys	Thr	Gly	Val	Tyr	Asn	Ile	Ile	Gly	Ser
		355					360					365			
Thr	Glu	Val	Lys	Asn	Glu	Ala	Lys	Ile	Ser	Ser	Gln				

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Ala Thr Lys Pro Thr Ser Tyr Pro Asn Leu Pro Lys Thr Gly Thr Tyr
435 440 445

Thr Phe Thr Lys Thr Val Asp Val Lys Ser Gln Pro Lys Val Ser Ser
450 455 460

Pro Val Glu Phe Asn Phe Gln Lys Gly Glu Lys Ile His Tyr Asp Gln
465 470 475 480

Val Leu Val Val Asp Gly His Gln Trp Ile Ser Tyr Lys Ser Tyr Ser
485 490 495

Gly Ile Arg Arg Tyr Ile Glu Ile
500

<210> SEQ ID NO 13
<211> LENGTH: 485
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 13

Met Lys Lys Gly Gln Val Asn Asp Thr Lys Gln Ser Tyr Ser Leu Arg
1 5 10 15

Lys Tyr Lys Phe Gly Leu Ala Ser Val Ile Leu Gly Ser Phe Ile Met
20 25 30

Val Thr Ser Pro Val Phe Ala Asp Gln Thr Thr Ser Val Gln Val Asn
35 40 45

Asn Gln Thr Gly Thr Ser Val Asp Ala Asn Asn Ser Ser Asn Glu Thr
50 55 60

Ser Ala Ser Ser Val Ile Thr Ser Asn Asn Asp Ser Val Gln Ala Ser
65 70 75 80

Asp Lys Val Val Asn Ser Gln Asn Thr Ala Thr Lys Asp Ile Thr Thr
85 90 95

Pro Leu Val Glu Thr Lys Pro Met Val Glu Lys Thr Leu Pro Glu Gln
100 105 110

Gly Asn Tyr Val Tyr Ser Lys Glu Thr Glu Val Lys Asn Thr Pro Ser
115 120 125

Lys Ser Ala Pro Val Ala Phe Tyr Ala Lys Lys Gly Asp Lys Val Phe
130 135 140

Tyr Asp Gln Val Phe Asn Lys Asp Asn Val Lys Trp Ile Ser Tyr Lys
145 150 155 160

Ser Phe Cys Gly Val Arg Arg Tyr Ala Ala Ile Glu Ser Leu Asp Pro
165 170 175

Ser Gly Gly Ser Glu Thr Lys Ala Pro Thr Pro Val Thr Asn Ser Gly
180 185 190

Ser Asn Asn Gln Glu Lys Ile Ala Thr Gln Gly Asn Tyr Thr Phe Ser
195 200 205

His Lys Val Glu Val Lys Asn Glu Ala Lys Val Ala Ser Pro Thr Gln
210 215 220

Phe Thr Leu Asp Lys Gly Asp Arg Ile Phe Tyr Asp Gln Ile Leu Thr
225 230 235 240

Ile Glu Gly Asn Gln Trp Leu Ser Tyr Lys Ser Phe Asn Gly Val Arg
245 250 255

Arg Phe Val Leu Leu Gly Lys Ala Ser Ser Val Glu Lys Thr Glu Asp
260 265 270

Lys Glu Lys Val Ser Pro Gln Pro Gln Ala Arg Ile Thr Lys Thr Gly
275 280 285

Arg Leu Thr Ile Ser Asn Glu Thr Thr Thr Gly Phe Asp Ile Leu Ile
290 295 300

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Thr Asn Ile Lys Asp Asp Asn Gly Ile Ala Ala Val Lys Val Pro Val
 305 310 315 320
 Trp Thr Glu Gln Gly Gly Gln Asp Asp Ile Lys Trp Tyr Thr Ala Val
 325 330 335
 Thr Thr Gly Asp Gly Asn Tyr Lys Val Ala Val Ser Phe Ala Asp His
 340 345 350
 Lys Asn Glu Lys Gly Leu Tyr Asn Ile His Leu Tyr Tyr Gln Glu Ala
 355 360 365
 Ser Gly Thr Leu Val Gly Val Thr Gly Thr Lys Val Thr Val Ala Gly
 370 375 380
 Thr Asn Ser Ser Gln Glu Pro Ile Glu Asn Gly Leu Ala Lys Thr Gly
 385 390 395 400
 Val Tyr Asn Ile Ile Gly Ser Thr Glu Val Lys Asn Glu Ala Lys Ile
 405 410 415
 Ser Ser Gln Thr Gln Phe Thr Leu Glu Lys Gly Asp Lys Ile Asn Tyr
 420 425 430
 Asp Gln Val Leu Thr Ala Asp Gly Tyr Gln Trp Ile Ser Tyr Lys Ser
 435 440 445
 Tyr Ser Gly Val Arg Arg Tyr Ile Pro Val Lys Lys Leu Thr Thr Ser
 450 455 460
 Ser Glu Lys Ala Lys Asp Glu Ala Thr Lys Pro Thr Ser Tyr Pro Asn
 465 470 475 480
 Leu Pro Lys Thr Gly
 485

<210> SEQ ID NO 14
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 14

Leu Thr Lys Thr Gly
 1 5

<210> SEQ ID NO 15
 <211> LENGTH: 480
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 15

Met Lys Lys Gly Gln Val Asn Asp Thr Lys Gln Ser Tyr Ser Leu Arg
 1 5 10 15
 Lys Tyr Lys Phe Gly Leu Ala Ser Val Ile Leu Gly Ser Phe Ile Met
 20 25 30
 Val Thr Ser Pro Val Phe Ala Asp Gln Thr Thr Ser Val Gln Val Asn
 35 40 45
 Asn Gln Thr Gly Thr Ser Val Asp Ala Asn Asn Ser Ser Asn Glu Thr
 50 55 60
 Ser Ala Ser Ser Val Ile Thr Ser Asn Asn Asp Ser Val Gln Ala Ser
 65 70 75 80
 Asp Lys Val Val Asn Ser Gln Asn Thr Ala Thr Lys Asp Ile Thr Thr
 85 90 95
 Pro Leu Val Glu Thr Lys Pro Met Val Glu Lys Thr Leu Pro Glu Gln
 100 105 110
 Gly Asn Tyr Val Tyr Ser Lys Glu Thr Glu Val Lys Asn Thr Pro Ser
 115 120 125

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Lys Ser Ala Pro Val Ala Phe Tyr Ala Lys Lys Gly Asp Lys Val Phe
 130 135 140
 Tyr Asp Gln Val Phe Asn Lys Asp Asn Val Lys Trp Ile Ser Tyr Lys
 145 150 155 160
 Ser Phe Cys Gly Val Arg Arg Tyr Ala Ala Ile Glu Ser Leu Asp Pro
 165 170 175
 Ser Gly Gly Ser Glu Thr Lys Ala Pro Thr Pro Val Thr Asn Ser Gly
 180 185 190
 Ser Asn Asn Gln Glu Lys Ile Ala Thr Gln Gly Asn Tyr Thr Phe Ser
 195 200 205
 His Lys Val Glu Val Lys Asn Glu Ala Lys Val Ala Ser Pro Thr Gln
 210 215 220
 Phe Thr Leu Asp Lys Gly Asp Arg Ile Phe Tyr Asp Gln Ile Leu Thr
 225 230 235 240
 Ile Glu Gly Asn Gln Trp Leu Ser Tyr Lys Ser Phe Asn Gly Val Arg
 245 250 255
 Arg Phe Val Leu Leu Gly Lys Ala Ser Ser Val Glu Lys Thr Glu Asp
 260 265 270
 Lys Glu Lys Val Ser Pro Gln Pro Gln Ala Arg Ile Thr Lys Thr Gly
 275 280 285
 Arg Leu Thr Ile Ser Asn Glu Thr Thr Thr Gly Phe Asp Ile Leu Ile
 290 295 300
 Thr Asn Ile Lys Asp Asp Asn Gly Ile Ala Ala Val Lys Val Pro Val
 305 310 315 320
 Trp Thr Glu Gln Gly Gly Gln Asp Asp Ile Lys Trp Tyr Thr Ala Val
 325 330 335
 Thr Thr Gly Asp Gly Asn Tyr Lys Val Ala Val Ser Phe Ala Asp His
 340 345 350
 Lys Asn Glu Lys Gly Leu Tyr Asn Ile His Leu Tyr Tyr Gln Glu Ala
 355 360 365
 Ser Gly Thr Leu Val Gly Val Thr Gly Thr Lys Val Thr Val Ala Gly
 370 375 380
 Thr Asn Ser Ser Gln Glu Pro Ile Glu Asn Gly Leu Ala Lys Thr Gly
 385 390 395 400
 Val Tyr Asn Ile Ile Gly Ser Thr Glu Val Lys Asn Glu Ala Lys Ile
 405 410 415
 Ser Ser Gln Thr Gln Phe Thr Leu Glu Lys Gly Asp Lys Ile Asn Tyr
 420 425 430
 Asp Gln Val Leu Thr Ala Asp Gly Tyr Gln Trp Ile Ser Tyr Lys Ser
 435 440 445
 Tyr Ser Gly Val Arg Arg Tyr Ile Pro Val Lys Lys Leu Thr Thr Ser
 450 455 460
 Ser Glu Lys Ala Lys Asp Glu Ala Thr Lys Pro Thr Ser Tyr Pro Asn
 465 470 475 480

<210> SEQ ID NO 16

<211> LENGTH: 446

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 16

Asp Gln Thr Thr Ser Val Gln Val Asn Asn Gln Thr Gly Thr Ser Val
 1 5 10 15

Asp Ala Asn Asn Ser Ser Asn Glu Thr Ser Ala Ser Ser Val Ile Thr

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20							25					30				
Ser	Asn	Asn	Asp	Ser	Val	Gln	Ala	Ser	Asp	Lys	Val	Val	Asn	Ser	Gln	
		35					40					45				
Asn	Thr	Ala	Thr	Lys	Asp	Ile	Thr	Thr	Pro	Leu	Val	Glu	Thr	Lys	Pro	
	50					55					60					
Met	Val	Glu	Lys	Thr	Leu	Pro	Glu	Gln	Gly	Asn	Tyr	Val	Tyr	Ser	Lys	
65					70					75					80	
Glu	Thr	Glu	Val	Lys	Asn	Thr	Pro	Ser	Lys	Ser	Ala	Pro	Val	Ala	Phe	
				85					90					95		
Tyr	Ala	Lys	Lys	Gly	Asp	Lys	Val	Phe	Tyr	Asp	Gln	Val	Phe	Asn	Lys	
			100					105					110			
Asp	Asn	Val	Lys	Trp	Ile	Ser	Tyr	Lys	Ser	Phe	Cys	Gly	Val	Arg	Arg	
		115					120					125				
Tyr	Ala	Ala	Ile	Glu	Ser	Leu	Asp	Pro	Ser	Gly	Gly	Ser	Glu	Thr	Lys	
	130					135					140					
Ala	Pro	Thr	Pro	Val	Thr	Asn	Ser	Gly	Ser	Asn	Asn	Gln	Glu	Lys	Ile	
145					150					155					160	
Ala	Thr	Gln	Gly	Asn	Tyr	Thr	Phe	Ser	His	Lys	Val	Glu	Val	Lys	Asn	
				165					170					175		
Glu	Ala	Lys	Val	Ala	Ser	Pro	Thr	Gln	Phe	Thr	Leu	Asp	Lys	Gly	Asp	
			180						185				190			
Arg	Ile	Phe	Tyr	Asp	Gln	Ile	Leu	Thr	Ile	Glu	Gly	Asn	Gln	Trp	Leu	
	195						200					205				
Ser	Tyr	Lys	Ser	Phe	Asn	Gly	Val	Arg	Arg	Phe	Val	Leu	Leu	Gly	Lys	
	210					215					220					
Ala	Ser	Ser	Val	Glu	Lys	Thr	Glu	Asp	Lys	Glu	Lys	Val	Ser	Pro	Gln	
225					230					235					240	
Pro	Gln	Ala	Arg	Ile	Thr	Lys	Thr	Gly	Arg	Leu	Thr	Ile	Ser	Asn	Glu	
				245					250					255		
Thr	Thr	Thr	Gly	Phe	Asp	Ile	Leu	Ile	Thr	Asn	Ile	Lys	Asp	Asp	Asn	
			260				265						270			
Gly	Ile	Ala	Ala	Val	Lys	Val	Pro	Val	Trp	Thr	Glu	Gln	Gly	Gly	Gln	
	275						280					285				
Asp	Asp	Ile	Lys	Trp	Tyr	Thr	Ala	Val	Thr	Thr	Gly	Asp	Gly	Asn	Tyr	
	290					295					300					
Lys	Val	Ala	Val	Ser	Phe	Ala	Asp	His	Lys	Asn	Glu	Lys	Gly	Leu	Tyr	
305					310					315					320	
Asn	Ile	His	Leu	Tyr	Tyr	Gln	Glu	Ala	Ser	Gly	Thr	Leu	Val	Gly	Val	
			325						330					335		
Thr	Gly	Thr	Lys	Val	Thr	Val	Ala	Gly	Thr	Asn	Ser	Ser	Gln	Glu	Pro	
			340				345						350			
Ile	Glu	Asn	Gly	Leu	Ala	Lys	Thr	Gly	Val	Tyr	Asn	Ile	Ile	Gly	Ser	
	355					360						365				
Thr	Glu	Val	Lys	Asn	Glu	Ala	Lys	Ile	Ser	Ser	Gln	Thr	Gln	Phe	Thr	
	370					375					380					
Leu	Glu	Lys	Gly	Asp	Lys	Ile	Asn	Tyr	Asp	Gln	Val	Leu	Thr	Ala	Asp	
385					390					395					400	
Gly	Tyr	Gln	Trp	Ile	Ser	Tyr	Lys	Ser	Tyr	Ser	Gly	Val	Arg	Arg	Tyr	
				405					410					415		
Ile	Pro	Val	Lys	Lys	Leu	Thr	Thr	Ser	Ser	Glu	Lys	Ala	Lys	Asp	Glu	
			420				425						430			
Ala	Thr	Lys	Pro	Thr	Ser	Tyr	Pro	Asn	Leu	Pro	Lys	Thr	Gly			
	435						440					445				

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<210> SEQ ID NO 17
<211> LENGTH: 441
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 17
Asp Gln Thr Thr Ser Val Gln Val Asn Asn Gln Thr Gly Thr Ser Val
 1          5          10          15
Asp Ala Asn Asn Ser Ser Asn Glu Thr Ser Ala Ser Ser Val Ile Thr
 20          25          30
Ser Asn Asn Asp Ser Val Gln Ala Ser Asp Lys Val Val Asn Ser Gln
 35          40          45
Asn Thr Ala Thr Lys Asp Ile Thr Thr Pro Leu Val Glu Thr Lys Pro
 50          55          60
Met Val Glu Lys Thr Leu Pro Glu Gln Gly Asn Tyr Val Tyr Ser Lys
 65          70          75          80
Glu Thr Glu Val Lys Asn Thr Pro Ser Lys Ser Ala Pro Val Ala Phe
 85          90          95
Tyr Ala Lys Lys Gly Asp Lys Val Phe Tyr Asp Gln Val Phe Asn Lys
100          105          110
Asp Asn Val Lys Trp Ile Ser Tyr Lys Ser Phe Cys Gly Val Arg Arg
115          120          125
Tyr Ala Ala Ile Glu Ser Leu Asp Pro Ser Gly Gly Ser Glu Thr Lys
130          135          140
Ala Pro Thr Pro Val Thr Asn Ser Gly Ser Asn Asn Gln Glu Lys Ile
145          150          155          160
Ala Thr Gln Gly Asn Tyr Thr Phe Ser His Lys Val Glu Val Lys Asn
165          170          175
Glu Ala Lys Val Ala Ser Pro Thr Gln Phe Thr Leu Asp Lys Gly Asp
180          185          190
Arg Ile Phe Tyr Asp Gln Ile Leu Thr Ile Glu Gly Asn Gln Trp Leu
195          200          205
Ser Tyr Lys Ser Phe Asn Gly Val Arg Arg Phe Val Leu Leu Gly Lys
210          215          220
Ala Ser Ser Val Glu Lys Thr Glu Asp Lys Glu Lys Val Ser Pro Gln
225          230          235          240
Pro Gln Ala Arg Ile Thr Lys Thr Gly Arg Leu Thr Ile Ser Asn Glu
245          250          255
Thr Thr Thr Gly Phe Asp Ile Leu Ile Thr Asn Ile Lys Asp Asp Asn
260          265          270
Gly Ile Ala Ala Val Lys Val Pro Val Trp Thr Glu Gln Gly Gly Gln
275          280          285
Asp Asp Ile Lys Trp Tyr Thr Ala Val Thr Thr Gly Asp Gly Asn Tyr
290          295          300
Lys Val Ala Val Ser Phe Ala Asp His Lys Asn Glu Lys Gly Leu Tyr
305          310          315          320
Asn Ile His Leu Tyr Tyr Gln Glu Ala Ser Gly Thr Leu Val Gly Val
325          330          335
Thr Gly Thr Lys Val Thr Val Ala Gly Thr Asn Ser Ser Gln Glu Pro
340          345          350
Ile Glu Asn Gly Leu Ala Lys Thr Gly Val Tyr Asn Ile Ile Gly Ser
355          360          365
Thr Glu Val Lys Asn Glu Ala Lys Ile Ser Ser Gln Thr Gln Phe Thr

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370	375	380	
Leu Glu Lys Gly Asp	Lys Ile Asn Tyr Asp	Gln Val Leu Thr Ala Asp	
385	390	395	400
Gly Tyr Gln Trp	Ile Ser Tyr Lys Ser	Tyr Ser Gly Val Arg Arg Tyr	
	405	410	415
Ile Pro Val Lys Lys Leu Thr Thr Ser Ser Glu Lys Ala Lys Asp Glu			
	420	425	430
Ala Thr Lys Pro Thr Ser Tyr Pro Asn			
	435	440	

<210> SEQ ID NO 18
 <211> LENGTH: 2670
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 18

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atgaaaaaga gacaaaaaat atggagaggg ttatcagtta ctttactaat cctgtcccaa    60
attccatttg gtatattggt acaagggtgaa acccaagata ccaatcaagc acttggaaaa    120
gtaattgtta aaaaaacggg agacaatgct acaccattag gcaaagcgac ttttgtgtta    180
aaaaatgaca atgataagtc agaaacaagt cagaaaacgg tagagggttc tggagaagca    240
acctttgaaa acataaaacc tggagactac acattaagag aagaaacagc accaattggt    300
tataaaaaaa ctgataaaac ctggaaagt aaagtgcag ataacggagc aacaataatc    360
gagggtatgg atgcagataa agcagagaaa cgaaaagaag ttttgaatgc ccaatatcca    420
aaatcagcta tttatgagga tacaaaagaa aattacccat tagttaatgt agagggttcc    480
aaagttgggt aacaatacaa agcattgaat ccaataaatg gaaaagatgg tcgaagagag    540
attgctgaag gttggttacc aaaaaaaatt acaggggtca atgatctcga taagaataaa    600
tataaaattg aattaactgt tgagggtaaa accactgttg aaacgaaaga acttaatcaa    660
ccactagatg tcgttgtgct attagataat tcaaatagta tgaataatga aagagccaat    720
aattctcaaa gagcattaaa agctggggaa gcagttgaaa agctgattga taaaattaca    780
tcaaataaag acaatagagt agctcttggt acatatgcct caaccatttt tgatgggtact    840
gaagcgaccg tatcaaaggg agttgccgat caaaatggta aagcgctgaa tgatagtgtg    900
tcatgggatt atcataaaac tactttttaca gcaactacac ataattacag ttattttaat    960
ttaacaaatg atgctaacga agttaatatt ctaaagtcaa gaattccaaa ggaagcggag    1020
catataaatg gggatcgcac gctctatcaa tttggtgcga catttactca aaaagctcta    1080
atgaaagcaa atgaaatatt agagacacaa agttctaatt ctagaaaaaa acttattttt    1140
cacgtaactg atgggtgtccc tacgatgtct tatgccataa attttaatcc ttatatatca    1200
acatcttacc aaaaccaggt taattctttt ttaaataaaa taccagatag aagtggattt    1260
ctccaagagg attttataat caatgggtgat gattatcaaa tagtaaaagg agatggagag    1320
agtttttaac tgttttcgga tagaaaagtt cctgttactg gaggaacgac acaagcagct    1380
tatcgagtac cgcaaatca actctctgta atgagtaatg agggatatgc aattaatagt    1440
ggatatatatt atctctattg gagagattac aactgggtct atccatttga tcctaagaca    1500
aagaaagttt ctgcaacgaa acaaatcaaa actcatggtg agccaacaac attatacttt    1560
aatggaaata taagacctaa aggttatgac atttttactg ttgggattgg tgtaaacgga    1620
gatcctgggt caactcctct tgaagctgag aaatttatgc aatcaatata aagtaaaaca    1680
gaaaattata ctaatgttga tgatacaaat aaaatttatg atgagctaaa taaatacttt    1740

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aaaacaattg ttgaggaaaa acattctatt gttgatggaa atgtgactga tctatggga 1800
gagatgattg aattccaatt aaaaaatggt caaagtttta cacatgatga ttacgttttg 1860
gttggaatg atggcagtc attaaaaat ggtgtggctc ttggtggacc aaacagtgat 1920
gggggaattt taaaagatgt tacagtgact tatgataaga catctcaaac catcaaaatc 1980
aatcatttga acttaggaag tggacaaaaa gtagttctta cctatgatgt acgtttaaaa 2040
gataactata taagtaacaa attttacaat acaataatc gtacaacgct aagtcggaag 2100
agtgaanaag aaccaaatat tttcgtgat ttcccaattc ccaaaattcg tgatgttcgt 2160
gagtttccgg tactaacat cagtaatcag aagaaaatgg gtgaggttga atttattaaa 2220
gttaataaag acaaacattc agaatcgctt ttgggagcta agtttcaact tcagatagaa 2280
aaagattttt ctgggtataa gcaatttggt ccagaggga gtgatgttac aacaaagaat 2340
gatggtaaaa tttattttaa agcacttcaa gatggtaact ataaattata tgaaatttca 2400
agtccagatg gctatataga ggtaaaaacg aaacctgttg tgacatttac aattcaaaat 2460
ggagaagtta cgaacctgaa agcagatcca aatgctaata aaaatcaaat cgggtatctt 2520
gaaggaaatg gtaaacatct tattaccaac actcccaaac gccaccagg tgtttttcct 2580
aaaacagggg gaattggtac aattgtctat atattagtgt gttctacttt tatgatactt 2640
accatttggt ctttcgctcg taaacaattg 2670

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<210> SEQ ID NO 19

<211> LENGTH: 890

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 19

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Met Lys Lys Arg Gln Lys Ile Trp Arg Gly Leu Ser Val Thr Leu Leu
 1         5         10        15
Ile Leu Ser Gln Ile Pro Phe Gly Ile Leu Val Gln Gly Glu Thr Gln
 20        25        30
Asp Thr Asn Gln Ala Leu Gly Lys Val Ile Val Lys Lys Thr Gly Asp
 35        40        45
Asn Ala Thr Pro Leu Gly Lys Ala Thr Phe Val Leu Lys Asn Asp Asn
 50        55        60
Asp Lys Ser Glu Thr Ser His Glu Thr Val Glu Gly Ser Gly Glu Ala
 65        70        75        80
Thr Phe Glu Asn Ile Lys Pro Gly Asp Tyr Thr Leu Arg Glu Glu Thr
 85        90        95
Ala Pro Ile Gly Tyr Lys Lys Thr Asp Lys Thr Trp Lys Val Lys Val
100       105       110
Ala Asp Asn Gly Ala Thr Ile Ile Glu Gly Met Asp Ala Asp Lys Ala
115       120       125
Glu Lys Arg Lys Glu Val Leu Asn Ala Gln Tyr Pro Lys Ser Ala Ile
130       135       140
Tyr Glu Asp Thr Lys Glu Asn Tyr Pro Leu Val Asn Val Glu Gly Ser
145       150       155       160
Lys Val Gly Glu Gln Tyr Lys Ala Leu Asn Pro Ile Asn Gly Lys Asp
165       170       175
Gly Arg Arg Glu Ile Ala Glu Gly Trp Leu Ser Lys Lys Ile Thr Gly
180       185       190
Val Asn Asp Leu Asp Lys Asn Lys Tyr Lys Ile Glu Leu Thr Val Glu
195       200       205

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Gly 210	Thr	Thr	Val	Glu	Thr	Lys	Glu	Leu	Asn	Gln	Pro	Leu	Asp	Val	
Val 225	Val	Leu	Leu	Asp	Asn	Ser	Asn	Ser	Met	Asn	Asn	Glu	Arg	Ala	Asn 240
Asn	Ser	Gln	Arg	Ala	Leu	Lys	Ala	Gly	Glu	Ala	Val	Glu	Lys	Leu	Ile 255
Asp	Lys	Ile	Thr	Ser	Asn	Lys	Asp	Asn	Arg	Val	Ala	Leu	Val	Thr	Tyr 270
Ala	Ser	Thr	Ile	Phe	Asp	Gly	Thr	Glu	Ala	Thr	Val	Ser	Lys	Gly	Val
Ala	Asp	Gln	Asn	Gly	Lys	Ala	Leu	Asn	Asp	Ser	Val	Ser	Trp	Asp	Tyr
His 305	Lys	Thr	Thr	Phe	Thr	Ala	Thr	Thr	His	Asn	Tyr	Ser	Tyr	Leu	Asn 320
Leu	Thr	Asn	Asp	Ala	Asn	Glu	Val	Asn	Ile	Leu	Lys	Ser	Arg	Ile	Pro 335
Lys	Glu	Ala	Glu	His	Ile	Asn	Gly	Asp	Arg	Thr	Leu	Tyr	Gln	Phe	Gly 350
Ala	Thr	Phe	Thr	Gln	Lys	Ala	Leu	Met	Lys	Ala	Asn	Glu	Ile	Leu	Glu 365
Thr	Gln	Ser	Ser	Asn	Ala	Arg	Lys	Lys	Leu	Ile	Phe	His	Val	Thr	Asp 370
Gly 385	Val	Pro	Thr	Met	Ser	Tyr	Ala	Ile	Asn	Phe	Asn	Pro	Tyr	Ile	Ser 400
Thr	Ser	Tyr	Gln	Asn	Gln	Phe	Asn	Ser	Phe	Leu	Asn	Lys	Ile	Pro	Asp 415
Arg	Ser	Gly	Ile	Leu	Gln	Glu	Asp	Phe	Ile	Ile	Asn	Gly	Asp	Asp	Tyr 420
Gln	Ile	Val	Lys	Gly	Asp	Gly	Glu	Ser	Phe	Lys	Leu	Phe	Ser	Asp	Arg 435
Lys 450	Val	Pro	Val	Thr	Gly	Gly	Thr	Thr	Gln	Ala	Ala	Tyr	Arg	Val	Pro 460
Gln 465	Asn	Gln	Leu	Ser	Val	Met	Ser	Asn	Glu	Gly	Tyr	Ala	Ile	Asn	Ser 475
Gly	Tyr	Ile	Tyr	Leu	Tyr	Trp	Arg	Asp	Tyr	Asn	Trp	Val	Tyr	Pro	Phe 485
Asp	Pro	Lys	Thr	Lys	Lys	Val	Ser	Ala	Thr	Lys	Gln	Ile	Lys	Thr	His 495
Gly	Glu	Pro	Thr	Thr	Leu	Tyr	Phe	Asn	Gly	Asn	Ile	Arg	Pro	Lys	Gly 500
Tyr 530	Asp	Ile	Phe	Thr	Val	Gly	Ile	Gly	Val	Asn	Gly	Asp	Pro	Gly	Ala 535
Thr 545	Pro	Leu	Glu	Ala	Glu	Lys	Phe	Met	Gln	Ser	Ile	Ser	Ser	Lys	Thr 550
Glu	Asn	Tyr	Thr	Asn	Val	Asp	Asp	Thr	Asn	Lys	Ile	Tyr	Asp	Glu	Leu 565
Asn	Lys	Tyr	Phe	Lys	Thr	Ile	Val	Glu	Glu	Lys	His	Ser	Ile	Val	Asp 575
Gly	Asn	Val	Thr	Asp	Pro	Met	Gly	Glu	Met	Ile	Glu	Phe	Gln	Leu	Lys 585
Asn	Gly	Gln	Ser	Phe	Thr	His	Asp	Asp	Tyr	Val	Leu	Val	Gly	Asn	Asp 595

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Gly	Ser	Gln	Leu	Lys	Asn	Gly	Val	Ala	Leu	Gly	Gly	Pro	Asn	Ser	Asp	625	630	635	640
Gly	Gly	Ile	Leu	Lys	Asp	Val	Thr	Val	Thr	Tyr	Asp	Lys	Thr	Ser	Gln	645	650	655	
Thr	Ile	Lys	Ile	Asn	His	Leu	Asn	Leu	Gly	Ser	Gly	Gln	Lys	Val	Val	660	665	670	
Leu	Thr	Tyr	Asp	Val	Arg	Leu	Lys	Asp	Asn	Tyr	Ile	Ser	Asn	Lys	Phe	675	680	685	
Tyr	Asn	Thr	Asn	Asn	Arg	Thr	Thr	Leu	Ser	Pro	Lys	Ser	Glu	Lys	Glu	690	695	700	
Pro	Asn	Thr	Ile	Arg	Asp	Phe	Pro	Ile	Pro	Lys	Ile	Arg	Asp	Val	Arg	705	710	715	720
Glu	Phe	Pro	Val	Leu	Thr	Ile	Ser	Asn	Gln	Lys	Lys	Met	Gly	Glu	Val	725	730	735	
Glu	Phe	Ile	Lys	Val	Asn	Lys	Asp	Lys	His	Ser	Glu	Ser	Leu	Leu	Gly	740	745	750	
Ala	Lys	Phe	Gln	Leu	Gln	Ile	Glu	Lys	Asp	Phe	Ser	Gly	Tyr	Lys	Gln	755	760	765	
Phe	Val	Pro	Glu	Gly	Ser	Asp	Val	Thr	Thr	Lys	Asn	Asp	Gly	Lys	Ile	770	775	780	
Tyr	Phe	Lys	Ala	Leu	Gln	Asp	Gly	Asn	Tyr	Lys	Leu	Tyr	Glu	Ile	Ser	785	790	795	800
Ser	Pro	Asp	Gly	Tyr	Ile	Glu	Val	Lys	Thr	Lys	Pro	Val	Val	Thr	Phe	805	810	815	
Thr	Ile	Gln	Asn	Gly	Glu	Val	Thr	Asn	Leu	Lys	Ala	Asp	Pro	Asn	Ala	820	825	830	
Asn	Lys	Asn	Gln	Ile	Gly	Tyr	Leu	Glu	Gly	Asn	Gly	Lys	His	Leu	Ile	835	840	845	
Thr	Asn	Thr	Pro	Lys	Arg	Pro	Pro	Gly	Val	Phe	Pro	Lys	Thr	Gly	Gly	850	855	860	
Ile	Gly	Thr	Ile	Val	Tyr	Ile	Leu	Val	Gly	Ser	Thr	Phe	Met	Ile	Leu	865	870	875	880
Thr	Ile	Cys	Ser	Phe	Arg	Arg	Lys	Gln	Leu							885	890		

<210> SEQ ID NO 20

<211> LENGTH: 862

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 20

Gly	Glu	Thr	Gln	Asp	Thr	Asn	Gln	Ala	Leu	Gly	Lys	Val	Ile	Val	Lys	1	5	10	15
Lys	Thr	Gly	Asp	Asn	Ala	Thr	Pro	Leu	Gly	Lys	Ala	Thr	Phe	Val	Leu	20	25	30	
Lys	Asn	Asp	Asn	Asp	Lys	Ser	Glu	Thr	Ser	His	Glu	Thr	Val	Glu	Gly	35	40	45	
Ser	Gly	Glu	Ala	Thr	Phe	Glu	Asn	Ile	Lys	Pro	Gly	Asp	Tyr	Thr	Leu	50	55	60	
Arg	Glu	Glu	Thr	Ala	Pro	Ile	Gly	Tyr	Lys	Lys	Thr	Asp	Lys	Thr	Trp	65	70	75	80
Lys	Val	Lys	Val	Ala	Asp	Asn	Gly	Ala	Thr	Ile	Ile	Glu	Gly	Met	Asp	85	90	95	
Ala	Asp	Lys	Ala	Glu	Lys	Arg	Lys	Glu	Val	Leu	Asn	Ala	Gln	Tyr	Pro	100	105	110	

-continued

Lys Ser Ala Ile Tyr Glu Asp Thr Lys Glu Asn Tyr Pro Leu Val Asn
 115 120 125
 Val Glu Gly Ser Lys Val Gly Glu Gln Tyr Lys Ala Leu Asn Pro Ile
 130 135 140
 Asn Gly Lys Asp Gly Arg Arg Glu Ile Ala Glu Gly Trp Leu Ser Lys
 145 150 155 160
 Lys Ile Thr Gly Val Asn Asp Leu Asp Lys Asn Lys Tyr Lys Ile Glu
 165 170 175
 Leu Thr Val Glu Gly Lys Thr Thr Val Glu Thr Lys Glu Leu Asn Gln
 180 185 190
 Pro Leu Asp Val Val Val Leu Leu Asp Asn Ser Asn Ser Met Asn Asn
 195 200 205
 Glu Arg Ala Asn Asn Ser Gln Arg Ala Leu Lys Ala Gly Glu Ala Val
 210 215 220
 Glu Lys Leu Ile Asp Lys Ile Thr Ser Asn Lys Asp Asn Arg Val Ala
 225 230 235 240
 Leu Val Thr Tyr Ala Ser Thr Ile Phe Asp Gly Thr Glu Ala Thr Val
 245 250 255
 Ser Lys Gly Val Ala Asp Gln Asn Gly Lys Ala Leu Asn Asp Ser Val
 260 265 270
 Ser Trp Asp Tyr His Lys Thr Thr Phe Thr Ala Thr Thr His Asn Tyr
 275 280 285
 Ser Tyr Leu Asn Leu Thr Asn Asp Ala Asn Glu Val Asn Ile Leu Lys
 290 295 300
 Ser Arg Ile Pro Lys Glu Ala Glu His Ile Asn Gly Asp Arg Thr Leu
 305 310 315 320
 Tyr Gln Phe Gly Ala Thr Phe Thr Gln Lys Ala Leu Met Lys Ala Asn
 325 330 335
 Glu Ile Leu Glu Thr Gln Ser Ser Asn Ala Arg Lys Lys Leu Ile Phe
 340 345 350
 His Val Thr Asp Gly Val Pro Thr Met Ser Tyr Ala Ile Asn Phe Asn
 355 360 365
 Pro Tyr Ile Ser Thr Ser Tyr Gln Asn Gln Phe Asn Ser Phe Leu Asn
 370 375 380
 Lys Ile Pro Asp Arg Ser Gly Ile Leu Gln Glu Asp Phe Ile Ile Asn
 385 390 395 400
 Gly Asp Asp Tyr Gln Ile Val Lys Gly Asp Gly Glu Ser Phe Lys Leu
 405 410 415
 Phe Ser Asp Arg Lys Val Pro Val Thr Gly Gly Thr Thr Gln Ala Ala
 420 425 430
 Tyr Arg Val Pro Gln Asn Gln Leu Ser Val Met Ser Asn Glu Gly Tyr
 435 440 445
 Ala Ile Asn Ser Gly Tyr Ile Tyr Leu Tyr Trp Arg Asp Tyr Asn Trp
 450 455 460
 Val Tyr Pro Phe Asp Pro Lys Thr Lys Lys Val Ser Ala Thr Lys Gln
 465 470 475 480
 Ile Lys Thr His Gly Glu Pro Thr Thr Leu Tyr Phe Asn Gly Asn Ile
 485 490 495
 Arg Pro Lys Gly Tyr Asp Ile Phe Thr Val Gly Ile Gly Val Asn Gly
 500 505 510
 Asp Pro Gly Ala Thr Pro Leu Glu Ala Glu Lys Phe Met Gln Ser Ile
 515 520 525

Ser	Ser	Lys	Thr	Glu	Asn	Tyr	Thr	Asn	Val	Asp	Asp	Thr	Asn	Lys	Ile
530						535					540				
Tyr	Asp	Glu	Leu	Asn	Lys	Tyr	Phe	Lys	Thr	Ile	Val	Glu	Glu	Lys	His
545					550					555					560
Ser	Ile	Val	Asp	Gly	Asn	Val	Thr	Asp	Pro	Met	Gly	Glu	Met	Ile	Glu
				565					570					575	
Phe	Gln	Leu	Lys	Asn	Gly	Gln	Ser	Phe	Thr	His	Asp	Asp	Tyr	Val	Leu
			580					585					590		
Val	Gly	Asn	Asp	Gly	Ser	Gln	Leu	Lys	Asn	Gly	Val	Ala	Leu	Gly	Gly
			595				600					605			
Pro	Asn	Ser	Asp	Gly	Gly	Ile	Leu	Lys	Asp	Val	Thr	Val	Thr	Tyr	Asp
610						615					620				
Lys	Thr	Ser	Gln	Thr	Ile	Lys	Ile	Asn	His	Leu	Asn	Leu	Gly	Ser	Gly
625					630					635					640
Gln	Lys	Val	Val	Leu	Thr	Tyr	Asp	Val	Arg	Leu	Lys	Asp	Asn	Tyr	Ile
				645					650					655	
Ser	Asn	Lys	Phe	Tyr	Asn	Thr	Asn	Asn	Arg	Thr	Thr	Leu	Ser	Pro	Lys
			660					665					670		
Ser	Glu	Lys	Glu	Pro	Asn	Thr	Ile	Arg	Asp	Phe	Pro	Ile	Pro	Lys	Ile
			675				680					685			
Arg	Asp	Val	Arg	Glu	Phe	Pro	Val	Leu	Thr	Ile	Ser	Asn	Gln	Lys	Lys
690						695					700				
Met	Gly	Glu	Val	Glu	Phe	Ile	Lys	Val	Asn	Lys	Asp	Lys	His	Ser	Glu
705					710					715					720
Ser	Leu	Leu	Gly	Ala	Lys	Phe	Gln	Leu	Gln	Ile	Glu	Lys	Asp	Phe	Ser
				725				730						735	
Gly	Tyr	Lys	Gln	Phe	Val	Pro	Glu	Gly	Ser	Asp	Val	Thr	Thr	Lys	Asn
			740					745					750		
Asp	Gly	Lys	Ile	Tyr	Phe	Lys	Ala	Leu	Gln	Asp	Gly	Asn	Tyr	Lys	Leu
			755				760					765			
Tyr	Glu	Ile	Ser	Ser	Pro	Asp	Gly	Tyr	Ile	Glu	Val	Lys	Thr	Lys	Pro
770						775					780				
Val	Val	Thr	Phe	Thr	Ile	Gln	Asn	Gly	Glu	Val	Thr	Asn	Leu	Lys	Ala
785					790					795					800
Asp	Pro	Asn	Ala	Asn	Lys	Asn	Gln	Ile	Gly	Tyr	Leu	Glu	Gly	Asn	Gly
				805					810					815	
Lys	His	Leu	Ile	Thr	Asn	Thr	Pro	Lys	Arg	Pro	Pro	Gly	Val	Phe	Pro
			820					825					830		
Lys	Thr	Gly	Gly	Ile	Gly	Thr	Ile	Val	Tyr	Ile	Leu	Val	Gly	Ser	Thr
			835					840				845			
Phe	Met	Ile	Leu	Thr	Ile	Cys	Ser	Phe	Arg	Arg	Lys	Gln	Leu		
850					855						860				

<400> SEQUENCE: 21

Met Lys Lys Arg Gln Lys Ile Trp Arg Gly Leu Ser Val Thr Leu Leu
1 5 10 15

Ile Leu Ser Gln Ile Pro Phe Gly Ile Leu Val Gln Gly Glu Thr Gln
20 25 30

Asp Thr Asn Gln Ala Leu Gly Lys Val Ile Val Lys Lys Thr Gly Asp
35 40 45

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Asn	Ala	Thr	Pro	Leu	Gly	Lys	Ala	Thr	Phe	Val	Leu	Lys	Asn	Asp	Asn
50						55					60				
Asp	Lys	Ser	Glu	Thr	Ser	His	Glu	Thr	Val	Glu	Gly	Ser	Gly	Glu	Ala
65					70					75					80
Thr	Phe	Glu	Asn	Ile	Lys	Pro	Gly	Asp	Tyr	Thr	Leu	Arg	Glu	Glu	Thr
				85					90					95	
Ala	Pro	Ile	Gly	Tyr	Lys	Lys	Thr	Asp	Lys	Thr	Trp	Lys	Val	Lys	Val
			100					105					110		
Ala	Asp	Asn	Gly	Ala	Thr	Ile	Ile	Glu	Gly	Met	Asp	Ala	Asp	Lys	Ala
		115					120					125			
Glu	Lys	Arg	Lys	Glu	Val	Leu	Asn	Ala	Gln	Tyr	Pro	Lys	Ser	Ala	Ile
	130					135					140				
Tyr	Glu	Asp	Thr	Lys	Glu	Asn	Tyr	Pro	Leu	Val	Asn	Val	Glu	Gly	Ser
145					150					155					160
Lys	Val	Gly	Glu	Gln	Tyr	Lys	Ala	Leu	Asn	Pro	Ile	Asn	Gly	Lys	Asp
				165				170						175	
Gly	Arg	Arg	Glu	Ile	Ala	Glu	Gly	Trp	Leu	Ser	Lys	Lys	Ile	Thr	Gly
			180					185					190		
Val	Asn	Asp	Leu	Asp	Lys	Asn	Lys	Tyr	Lys	Ile	Glu	Leu	Thr	Val	Glu
		195					200					205			
Gly	Lys	Thr	Thr	Val	Glu	Thr	Lys	Glu	Leu	Asn	Gln	Pro	Leu	Asp	Val
	210					215					220				
Val	Val	Leu	Leu	Asp	Asn	Ser	Asn	Ser	Met	Asn	Asn	Glu	Arg	Ala	Asn
225					230					235					240
Asn	Ser	Gln	Arg	Ala	Leu	Lys	Ala	Gly	Glu	Ala	Val	Glu	Lys	Leu	Ile
				245				250						255	
Asp	Lys	Ile	Thr	Ser	Asn	Lys	Asp	Asn	Arg	Val	Ala	Leu	Val	Thr	Tyr
			260					265					270		
Ala	Ser	Thr	Ile	Phe	Asp	Gly	Thr	Glu	Ala	Thr	Val	Ser	Lys	Gly	Val
		275					280					285			
Ala	Asp	Gln	Asn	Gly	Lys	Ala	Leu	Asn	Asp	Ser	Val	Ser	Trp	Asp	Tyr
	290				295					300					
His	Lys	Thr	Thr	Phe	Thr	Ala	Thr	Thr	His	Asn	Tyr	Ser	Tyr	Leu	Asn
305					310					315					320
Leu	Thr	Asn	Asp	Ala	Asn	Glu	Val	Asn	Ile	Leu	Lys	Ser	Arg	Ile	Pro
				325				330						335	
Lys	Glu	Ala	Glu	His	Ile	Asn	Gly	Asp	Arg	Thr	Leu	Tyr	Gln	Phe	Gly
		340						345					350		
Ala	Thr	Phe	Thr	Gln	Lys	Ala	Leu	Met	Lys	Ala	Asn	Glu	Ile	Leu	Glu
		355					360					365			
Thr	Gln	Ser	Ser	Asn	Ala	Arg	Lys	Lys	Leu	Ile	Phe	His	Val	Thr	Asp
	370				375					380					
Gly	Val	Pro	Thr	Met	Ser	Tyr	Ala	Ile	Asn	Phe	Asn	Pro	Tyr	Ile	Ser
385					390					395					400
Thr	Ser	Tyr	Gln	Asn	Gln	Phe	Asn	Ser	Phe	Leu	Asn	Lys	Ile	Pro	Asp
				405					410					415	
Arg	Ser	Gly	Ile	Leu	Gln	Glu	Asp	Phe	Ile	Ile	Asn	Gly	Asp	Asp	Tyr
			420					425					430		
Gln	Ile	Val	Lys	Gly	Asp	Gly	Glu	Ser	Phe	Lys	Leu	Phe	Ser	Asp	Arg
	435						440					445			
Lys	Val	Pro	Val	Thr	Gly	Gly	Thr	Thr	Gln	Ala	Ala	Tyr	Arg	Val	Pro
	450					455					460				

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Gln	Asn	Gln	Leu	Ser	Val	Met	Ser	Asn	Glu	Gly	Tyr	Ala	Ile	Asn	Ser	465	470	475	480
Gly	Tyr	Ile	Tyr	Leu	Tyr	Trp	Arg	Asp	Tyr	Asn	Trp	Val	Tyr	Pro	Phe	485	490	495	
Asp	Pro	Lys	Thr	Lys	Lys	Val	Ser	Ala	Thr	Lys	Gln	Ile	Lys	Thr	His	500	505	510	
Gly	Glu	Pro	Thr	Thr	Leu	Tyr	Phe	Asn	Gly	Asn	Ile	Arg	Pro	Lys	Gly	515	520	525	
Tyr	Asp	Ile	Phe	Thr	Val	Gly	Ile	Gly	Val	Asn	Gly	Asp	Pro	Gly	Ala	530	535	540	
Thr	Pro	Leu	Glu	Ala	Glu	Lys	Phe	Met	Gln	Ser	Ile	Ser	Ser	Lys	Thr	545	550	555	560
Glu	Asn	Tyr	Thr	Asn	Val	Asp	Asp	Thr	Asn	Lys	Ile	Tyr	Asp	Glu	Leu	565	570	575	
Asn	Lys	Tyr	Phe	Lys	Thr	Ile	Val	Glu	Glu	Lys	His	Ser	Ile	Val	Asp	580	585	590	
Gly	Asn	Val	Thr	Asp	Pro	Met	Gly	Glu	Met	Ile	Glu	Phe	Gln	Leu	Lys	595	600	605	
Asn	Gly	Gln	Ser	Phe	Thr	His	Asp	Asp	Tyr	Val	Leu	Val	Gly	Asn	Asp	610	615	620	
Gly	Ser	Gln	Leu	Lys	Asn	Gly	Val	Ala	Leu	Gly	Gly	Pro	Asn	Ser	Asp	625	630	635	640
Gly	Gly	Ile	Leu	Lys	Asp	Val	Thr	Val	Thr	Tyr	Asp	Lys	Thr	Ser	Gln	645	650	655	
Thr	Ile	Lys	Ile	Asn	His	Leu	Asn	Leu	Gly	Ser	Gly	Gln	Lys	Val	Val	660	665	670	
Leu	Thr	Tyr	Asp	Val	Arg	Leu	Lys	Asp	Asn	Tyr	Ile	Ser	Asn	Lys	Phe	675	680	685	
Tyr	Asn	Thr	Asn	Asn	Arg	Thr	Thr	Leu	Ser	Pro	Lys	Ser	Glu	Lys	Glu	690	695	700	
Pro	Asn	Thr	Ile	Arg	Asp	Phe	Pro	Ile	Pro	Lys	Ile	Arg	Asp	Val	Arg	705	710	715	720
Glu	Phe	Pro	Val	Leu	Thr	Ile	Ser	Asn	Gln	Lys	Lys	Met	Gly	Glu	Val	725	730	735	
Glu	Phe	Ile	Lys	Val	Asn	Lys	Asp	Lys	His	Ser	Glu	Ser	Leu	Leu	Gly	740	745	750	
Ala	Lys	Phe	Gln	Leu	Gln	Ile	Glu	Lys	Asp	Phe	Ser	Gly	Tyr	Lys	Gln	755	760	765	
Phe	Val	Pro	Glu	Gly	Ser	Asp	Val	Thr	Thr	Lys	Asn	Asp	Gly	Lys	Ile	770	775	780	
Tyr	Phe	Lys	Ala	Leu	Gln	Asp	Gly	Asn	Tyr	Lys	Leu	Tyr	Glu	Ile	Ser	785	790	795	800
Ser	Pro	Asp	Gly	Tyr	Ile	Glu	Val	Lys	Thr	Lys	Pro	Val	Val	Thr	Phe	805	810	815	
Thr	Ile	Gln	Asn	Gly	Glu	Val	Thr	Asn	Leu	Lys	Ala	Asp	Pro	Asn	Ala	820	825	830	
Asn	Lys	Asn	Gln	Ile	Gly	Tyr	Leu	Glu	Gly	Asn	Gly	Lys	His	Leu	Ile	835	840	845	
Thr	Asn	Thr														850			

<210> SEQ ID NO 22

<211> LENGTH: 823

<212> TYPE: PRT

-continued

<213> ORGANISM: *Streptococcus agalactiae*

<400> SEQUENCE: 22

Gly Glu Thr Gln Asp Thr Asn Gln Ala Leu Gly Lys Val Ile Val Lys
 1 5 10 15
 Lys Thr Gly Asp Asn Ala Thr Pro Leu Gly Lys Ala Thr Phe Val Leu
 20 25 30
 Lys Asn Asp Asn Asp Lys Ser Glu Thr Ser His Glu Thr Val Glu Gly
 35 40 45
 Ser Gly Glu Ala Thr Phe Glu Asn Ile Lys Pro Gly Asp Tyr Thr Leu
 50 55 60
 Arg Glu Glu Thr Ala Pro Ile Gly Tyr Lys Lys Thr Asp Lys Thr Trp
 65 70 75 80
 Lys Val Lys Val Ala Asp Asn Gly Ala Thr Ile Ile Glu Gly Met Asp
 85 90 95
 Ala Asp Lys Ala Glu Lys Arg Lys Glu Val Leu Asn Ala Gln Tyr Pro
 100 105 110
 Lys Ser Ala Ile Tyr Glu Asp Thr Lys Glu Asn Tyr Pro Leu Val Asn
 115 120 125
 Val Glu Gly Ser Lys Val Gly Glu Gln Tyr Lys Ala Leu Asn Pro Ile
 130 135 140
 Asn Gly Lys Asp Gly Arg Arg Glu Ile Ala Glu Gly Trp Leu Ser Lys
 145 150 155 160
 Lys Ile Thr Gly Val Asn Asp Leu Asp Lys Asn Lys Tyr Lys Ile Glu
 165 170 175
 Leu Thr Val Glu Gly Lys Thr Thr Val Glu Thr Lys Glu Leu Asn Gln
 180 185 190
 Pro Leu Asp Val Val Val Leu Leu Asp Asn Ser Asn Ser Met Asn Asn
 195 200 205
 Glu Arg Ala Asn Asn Ser Gln Arg Ala Leu Lys Ala Gly Glu Ala Val
 210 215 220
 Glu Lys Leu Ile Asp Lys Ile Thr Ser Asn Lys Asp Asn Arg Val Ala
 225 230 235 240
 Leu Val Thr Tyr Ala Ser Thr Ile Phe Asp Gly Thr Glu Ala Thr Val
 245 250 255
 Ser Lys Gly Val Ala Asp Gln Asn Gly Lys Ala Leu Asn Asp Ser Val
 260 265 270
 Ser Trp Asp Tyr His Lys Thr Thr Phe Thr Ala Thr Thr His Asn Tyr
 275 280 285
 Ser Tyr Leu Asn Leu Thr Asn Asp Ala Asn Glu Val Asn Ile Leu Lys
 290 295 300
 Ser Arg Ile Pro Lys Glu Ala Glu His Ile Asn Gly Asp Arg Thr Leu
 305 310 315 320
 Tyr Gln Phe Gly Ala Thr Phe Thr Gln Lys Ala Leu Met Lys Ala Asn
 325 330 335
 Glu Ile Leu Glu Thr Gln Ser Ser Asn Ala Arg Lys Lys Leu Ile Phe
 340 345 350
 His Val Thr Asp Gly Val Pro Thr Met Ser Tyr Ala Ile Asn Phe Asn
 355 360 365
 Pro Tyr Ile Ser Thr Ser Tyr Gln Asn Gln Phe Asn Ser Phe Leu Asn
 370 375 380
 Lys Ile Pro Asp Arg Ser Gly Ile Leu Gln Glu Asp Phe Ile Ile Asn
 385 390 395 400

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820

<210> SEQ ID NO 23
 <211> LENGTH: 549
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 23

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atgaaaaaac aaaaactatt actgcttatt ggaggcttat taataatgat aatgatgaca      60
gcatgtaagg attcaaaaat cccagaaaaac cgcacaaaagg aagagtacca agctgaacaa    120
aattttaaac cgttttttga gtttttagca caaaaagata aagatttgag caaaatacaa    180
aaatacttac tattagtatc ggattcaggt gatgcattag atttagaata tttctatagt    240
attcaagatt taaaaaaaa taaggattta gggaagtttg aaacaagaaa aagtcaaata    300
gaaaagccgg gtggctataa tgagtttagaa aataaagagg tcccatttga atattttaaa    360
aataatatag tttatccaaa aggaaaaccg aatattacat ttgatgactt tattatcgga    420
gcaatggata ctaaagaatt aaaagaatta aaaaaattaa aagtaaaaag ttatttatta    480
aaacatccgg aaactgagtt gaaagatata acatatgaat tgccgacaca gtcgaagctt    540
attaaaaaa                                     549
  
```

<210> SEQ ID NO 24
 <211> LENGTH: 183
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 24

```

Met Lys Lys Gln Lys Leu Leu Leu Leu Ile Gly Gly Leu Leu Ile Met
 1         5             10             15
Ile Met Met Thr Ala Cys Lys Asp Ser Lys Ile Pro Glu Asn Arg Thr
 20         25             30
Lys Glu Glu Tyr Gln Ala Glu Gln Asn Phe Lys Pro Phe Phe Glu Phe
 35         40             45
Leu Ala Gln Lys Asp Lys Asp Leu Ser Lys Ile Gln Lys Tyr Leu Leu
 50         55             60
Leu Val Ser Asp Ser Gly Asp Ala Leu Asp Leu Glu Tyr Phe Tyr Ser
 65         70             75             80
Ile Gln Asp Leu Lys Lys Asn Lys Asp Leu Gly Lys Phe Glu Thr Arg
 85         90             95
Lys Ser Gln Ile Glu Lys Pro Gly Gly Tyr Asn Glu Leu Glu Asn Lys
100        105            110
Glu Val Pro Phe Glu Tyr Phe Lys Asn Asn Ile Val Tyr Pro Lys Gly
115        120            125
Lys Pro Asn Ile Thr Phe Asp Asp Phe Ile Ile Gly Ala Met Asp Thr
130        135            140
Lys Glu Leu Lys Glu Leu Lys Lys Leu Lys Val Lys Ser Tyr Leu Leu
145        150            155            160
Lys His Pro Glu Thr Glu Leu Lys Asp Ile Thr Tyr Glu Leu Pro Thr
165        170            175
Gln Ser Lys Leu Ile Lys Lys
180
  
```

<210> SEQ ID NO 25
 <211> LENGTH: 161
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

-continued

<400> SEQUENCE: 25

Lys Asp Ser Lys Ile Pro Glu Asn Arg Thr Lys Glu Glu Tyr Gln Ala
 1 5 10 15
 Glu Gln Asn Phe Lys Pro Phe Phe Glu Phe Leu Ala Gln Lys Asp Lys
 20 25 30
 Asp Leu Ser Lys Ile Gln Lys Tyr Leu Leu Leu Val Ser Asp Ser Gly
 35 40 45
 Asp Ala Leu Asp Leu Glu Tyr Phe Tyr Ser Ile Gln Asp Leu Lys Lys
 50 55 60
 Asn Lys Asp Leu Gly Lys Phe Glu Thr Arg Lys Ser Gln Ile Glu Lys
 65 70 75 80
 Pro Gly Gly Tyr Asn Glu Leu Glu Asn Lys Glu Val Pro Phe Glu Tyr
 85 90 95
 Phe Lys Asn Asn Ile Val Tyr Pro Lys Gly Lys Pro Asn Ile Thr Phe
 100 105 110
 Asp Asp Phe Ile Ile Gly Ala Met Asp Thr Lys Glu Leu Lys Glu Leu
 115 120 125
 Lys Lys Leu Lys Val Lys Ser Tyr Leu Leu Lys His Pro Glu Thr Glu
 130 135 140
 Leu Lys Asp Ile Thr Tyr Glu Leu Pro Thr Gln Ser Lys Leu Ile Lys
 145 150 155 160
 Lys

<210> SEQ ID NO 26

<211> LENGTH: 3402

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 26

ttgcgtaaaa aacaaaaact accatttgat aaacttgcca ttgcgcttat atctacgagc 60
 atcttgctca atgcacaatc agacattaaa gcaaatactg tgacagaaga cactcctgct 120
 accgaacaag ccgtagaacc cccacaacca atagcagttt ctgaggaatc acgatcatca 180
 aaggaaacta aaacctcaca aactcctagt gatgtaggag aaacagtagc agatgacgct 240
 aatgatctag cccctcaagc tcctgctaaa actgctgata caccagcaac ctcaaaagcg 300
 actattaggg atttgaacga ccttctcat gtcaaaaccc tgcaggaaaa agcaggcaag 360
 ggagctggga ccgttgttgc agtgattgat gctggttttg ataaaaatca tgaagcgtgg 420
 cgcttaacag acaaaactaa agcacgttac caatcaaaag aaaatcttga aaaagctaaa 480
 aaagagcacg gtattaccta tggcgagtgg gtcaatgata aggttgctta ttaccacgac 540
 tatagtaaa atggtaaaaa cgctgttgat caagaacacg gcacacacgt gtcagggatc 600
 ttgtcaggaa atgctccatc tgaaatgaaa gaaccttacc gcctagaagg tgcgatgcct 660
 gaggtcaat tgcttttgat gcgtgtcgaa attgtaaatg gactagcaga ctatgctcgt 720
 aactacgctc aagctatcag agatgctgtc aacttgggag ctaaggtgat taatatgagc 780
 tttggtaatg ctgcactagc ttacgccaac cttccagacg aaacaaaaaa agcctttgac 840
 tatgccaaat caaaagggtg tagcattgtg acctcagctg gtaatgatag tagctttggg 900
 ggcaagcccc gtctacctct agcagatcat cctgattatg ggggtggttg gacacctgca 960
 gcggcagatt caacattgac agttgcttct tacagcccag ataacagct cactgaaact 1020
 gctacgggtca aaacagacga tcatcaagat aaagaaatgc ctgttatattc aacaaaccgt 1080

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tttgagccaa	acaaggctta	cgactatgct	tatgctaatac	gtggtacgaa	agaggatgat	1140
tttaaggatg	tcgaaggtaa	gattgccctt	attgaacgtg	gcgatattga	tttcaaagat	1200
aagattgcaa	acgctaaaaa	agctgggtgct	gtaggggtct	tgatctatga	caatcaagac	1260
aagggttcc	cgattgaatt	gccaaatgtt	gaccagatgc	ctgcggcctt	tatcagtcga	1320
agagacggtc	tcttattaaa	agacaatccc	ccaaaaacca	ttaccttcaa	tgcgacacct	1380
aaggtattgc	caacagcaag	tggcacccaaa	ctaagccgct	tctcaagctg	gggtctgaca	1440
gctgacggca	atattaaacc	ggatattgca	gcacccggcc	aagatatttt	gtcatcagtg	1500
gctaacaaca	agtatgccaa	actttctgga	actagtatgt	ctgcaccatt	ggtagcgggt	1560
atcatgggac	tggtgcaaaa	gcaatatgag	acacagtatc	ctgatatgac	accatcagag	1620
cgtcttgatt	tagctaagaa	agtattgatg	agctcagcaa	ctgccctata	tgatgaagat	1680
gaaaaagctt	atttttctcc	tcgccaacag	ggagcaggag	cagtcgatgc	taaaaaagct	1740
tcagcagcaa	cgatgtatgt	aacagataag	gacaatacct	caagcaaggt	tcacctgaac	1800
aatgtttctg	ataaatattga	agtaacagta	acagttcaca	acaaatctga	taaacctcaa	1860
gagttgtatt	accaagtaac	tgttcaaaaca	gataaagtag	atggaaaaaca	ctttgccttg	1920
gctcctaag	cattgtatga	gacatcatgg	caaaaaatca	caattccagc	caatagcagc	1980
aaacaagtca	cggttccaat	cgatgctagt	cgatttagca	aggacttgct	tgcccaaag	2040
aaaaatggct	atttcttaga	aggttttgtt	cgtttcaaac	aagatcctac	aaaagaagag	2100
cttatgagca	ttccatatat	tggtttccga	ggtgatattg	gcaatctgtc	agccttagaa	2160
aaaccaatct	atgatagcaa	agacggtagc	agctactatc	atgaagcaaa	tagtgatgcc	2220
aaagaccaat	tagatgggtga	tggattacag	ttttacgctc	tgaaaaataa	ctttacagca	2280
cttaccacag	agtctaacc	atggaagatt	attaaagctg	tcaagaagg	gggtgaaaac	2340
atagaggata	tcgaatcttc	agagatcaca	gaaaccattt	ttgcaggtag	ttttgcaaaa	2400
caagacgatg	atagccacta	ctatatccac	cgtcacgcta	atggcaaac	atatgctgcg	2460
atctctccaa	atggggacgg	taacagagat	tatgtccaat	tccaaggtag	tttcttgctg	2520
aatgctaaaa	accttggtgc	tgaagtcttg	gacaaagaag	gaaatgttgt	ttggacaagt	2580
gaggtaaccg	agcaagttgt	taaaaactac	aacaatgact	tggcaagcac	acttggttca	2640
acccgttttg	aaaaaacgcg	ttgggacggg	aaagataaag	acggcaaggt	tggtgctaac	2700
ggaacctaca	cctatcgtgt	tcgctacacg	ccgattagct	cagggtgcaa	agaacaacac	2760
actgattttg	atgtgatgtg	agacaatacg	acacctgaag	tcgcaacatc	ggcaacattc	2820
tcaacagaag	atagtcgttt	gacacttgca	tctaaaccaa	aaaccagcca	accggtttac	2880
cgtgagcgta	ttgcttacac	ttatatggat	gaggatctgc	caacaacaga	gtatatttct	2940
ccaaatgaag	atgggtacctt	tactcttctc	gaagaggctg	aaacaatgga	aggcgctact	3000
gttcatttga	aaatgtcaga	ctttacttat	gttggtgaag	atatggctgg	taacatcact	3060
tatacaccag	tgactaagct	attggagggc	cactctaata	agccagaaca	agacggttca	3120
gatcaagcac	cagacaagaa	accagaagct	aaaccagaac	aagacgggtc	aggtcaaaaa	3180
ccagataaaa	aaaaaagaac	taaaccagaa	aaagatagtt	cagggtcaaac	accaggtaaa	3240
actcctcaaa	aagggtcaatc	ttctcgtact	ctagagaaac	gatcttctaa	gcgtgcttta	3300
gctacaaaa	catcaacaag	agatcagtta	ccaacgacta	atgacaagga	tacaaatcgt	3360
ttacatctcc	ttaagttagt	tatgaccact	ttcttcttgg	ga		3402

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<210> SEQ ID NO 27
<211> LENGTH: 1134
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 27

Met Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 1           5           10           15

Ile Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
      20           25           30

Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Pro Pro
      35           40           45

Gln Pro Ile Ala Val Ser Glu Glu Ser Arg Ser Ser Lys Glu Thr Lys
      50           55           60

Thr Ser Gln Thr Pro Ser Asp Val Gly Glu Thr Val Ala Asp Asp Ala
      65           70           75           80

Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
      85           90           95

Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser His Val Lys
      100          105          110

Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
      115          120          125

Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
      130          135          140

Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asn Leu Glu Lys Ala Lys
      145          150          155          160

Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
      165          170          175

Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Asn Ala Val Asp Gln Glu
      180          185          190

His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
      195          200          205

Met Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
      210          215          220

Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
      225          230          235          240

Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val
      245          250          255

Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
      260          265          270

Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
      275          280          285

Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Pro Arg
      290          295          300

Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
      305          310          315          320

Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
      325          330          335

Leu Thr Glu Thr Ala Thr Val Lys Thr Asp Asp His Gln Asp Lys Glu
      340          345          350

Met Pro Val Ile Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
      355          360          365

Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val
      370          375          380

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Glu 385	Gly	Lys	Ile	Ala	Leu 390	Ile	Glu	Arg	Gly	Asp 395	Ile	Asp	Phe	Lys	Asp 400
Lys	Ile	Ala	Asn 405	Ala	Lys	Lys	Ala	Gly	Ala 410	Val	Gly	Val	Leu	Ile	Tyr 415
Asp	Asn	Gln	Asp 420	Lys	Gly	Phe	Pro	Ile	Glu 425	Leu	Pro	Asn	Val	Asp	Gln 430
Met	Pro	Ala 435	Ala	Phe	Ile	Ser	Arg	Arg	Asp 440	Gly	Leu	Leu	Leu	Lys	Asp 445
Asn	Pro	Pro	Lys	Thr	Ile 450	Thr	Phe	Asn	Ala 455	Thr	Pro	Lys	Val	Leu	Pro 460
Thr	Ala	Ser	Gly	Thr	Lys 465	Leu	Ser	Arg	Phe 470	Ser	Ser	Trp	Gly	Leu	Thr 480
Ala	Asp	Gly	Asn 485	Ile	Lys	Pro	Asp	Ile	Ala 490	Ala	Pro	Gly	Gln	Asp	Ile 495
Leu	Ser	Ser	Val 500	Ala	Asn	Asn	Lys	Tyr	Ala 505	Lys	Leu	Ser	Gly	Thr	Ser 510
Met	Ser	Ala 515	Pro	Leu	Val	Ala	Gly 520	Ile	Met	Gly	Leu	Leu	Gln	Lys	Gln 525
Tyr	Glu	Thr	Gln	Tyr	Pro 530	Asp	Met	Thr	Pro 535	Ser	Glu	Arg	Leu	Asp	Leu 540
Ala	Lys	Lys	Val	Leu	Met 545	Ser	Ser	Ala	Thr 550	Ala	Leu	Tyr	Asp	Glu	Asp 560
Glu	Lys	Ala	Tyr	Phe 565	Ser	Pro	Arg	Gln	Gln 570	Gly	Ala	Gly	Ala	Val	Asp 575
Ala	Lys	Lys	Ala 580	Ser	Ala	Ala	Thr	Met	Tyr 585	Val	Thr	Asp	Lys	Asp	Asn 590
Thr	Ser	Ser	Lys 595	Val	His	Leu	Asn 600	Asn	Val	Ser	Asp	Lys	Phe	Glu	Val 605
Thr	Val	Thr	Val	His	Asn 610	Lys	Ser	Asp	Lys 615	Pro	Gln	Glu	Leu	Tyr	Tyr 620
Gln	Val	Thr	Val	Gln	Thr 625	Asp	Lys	Val	Asp 630	Gly	Lys	His	Phe	Ala	Leu 640
Ala	Pro	Lys	Ala 645	Leu	Tyr	Glu	Thr	Ser	Trp 650	Gln	Lys	Ile	Thr	Ile	Pro 655
Ala	Asn	Ser	Ser 660	Lys	Gln	Val	Thr	Val 665	Pro	Ile	Asp	Ala	Ser	Arg	Phe 670
Ser	Lys	Asp 675	Leu	Leu	Ala	Gln	Met 680	Lys	Asn	Gly	Tyr	Phe	Leu	Glu	Gly 685
Phe	Val	Arg	Phe 690	Lys	Gln	Asp	Pro 695	Thr	Lys	Glu	Glu	Leu	Met	Ser	Ile 700
Pro	Tyr	Ile	Gly	Phe 705	Arg	Gly	Asp 710	Phe	Gly	Asn 715	Leu	Ser	Ala	Leu	Glu 720
Lys	Pro	Ile	Tyr	Asp 725	Ser	Lys	Asp	Gly	Ser 730	Ser	Tyr	Tyr	His	Glu	Ala 735
Asn	Ser	Asp	Ala 740	Lys	Asp	Gln	Leu	Asp 745	Gly	Asp	Gly	Leu	Gln	Phe	Tyr 750
Ala	Leu	Lys	Asn 755	Asn	Phe	Thr	Ala 760	Leu	Thr	Thr	Glu	Ser	Asn	Pro	Trp 765
Thr	Ile	Ile	Lys	Ala 770	Val	Lys	Glu 775	Gly	Val	Glu	Asn	Ile	Glu	Asp	Ile 780
Glu	Ser	Ser	Glu	Ile 785	Thr	Glu	Thr 790	Ile	Phe	Ala 795	Gly	Thr	Phe	Ala	Lys 800
Gln	Asp	Asp	Asp	Ser	His	Tyr	Tyr	Ile	His	Arg	His	Ala	Asn	Gly	Lys

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805					810					815					
Pro	Tyr	Ala	Ala	Ile	Ser	Pro	Asn	Gly	Asp	Gly	Asn	Arg	Asp	Tyr	Val
		820						825					830		
Gln	Phe	Gln	Gly	Thr	Phe	Leu	Arg	Asn	Ala	Lys	Asn	Leu	Val	Ala	Glu
		835					840					845			
Val	Leu	Asp	Lys	Glu	Gly	Asn	Val	Val	Trp	Thr	Ser	Glu	Val	Thr	Glu
	850					855					860				
Gln	Val	Val	Lys	Asn	Tyr	Asn	Asn	Asp	Leu	Ala	Ser	Thr	Leu	Gly	Ser
865				870					875					880	
Thr	Arg	Phe	Glu	Lys	Thr	Arg	Trp	Asp	Gly	Lys	Asp	Lys	Asp	Gly	Lys
			885					890						895	
Val	Val	Ala	Asn	Gly	Thr	Tyr	Thr	Tyr	Arg	Val	Arg	Tyr	Thr	Pro	Ile
			900					905					910		
Ser	Ser	Gly	Ala	Lys	Glu	Gln	His	Thr	Asp	Phe	Asp	Val	Ile	Val	Asp
		915					920					925			
Asn	Thr	Thr	Pro	Glu	Val	Ala	Thr	Ser	Ala	Thr	Phe	Ser	Thr	Glu	Asp
		930				935					940				
Ser	Arg	Leu	Thr	Leu	Ala	Ser	Lys	Pro	Lys	Thr	Ser	Gln	Pro	Val	Tyr
945				950					955					960	
Arg	Glu	Arg	Ile	Ala	Tyr	Thr	Tyr	Met	Asp	Glu	Asp	Leu	Pro	Thr	Thr
			965					970						975	
Glu	Tyr	Ile	Ser	Pro	Asn	Glu	Asp	Gly	Thr	Phe	Thr	Leu	Pro	Glu	Glu
		980					985					990			
Ala	Glu	Thr	Met	Glu	Gly	Ala	Thr	Val	Pro	Leu	Lys	Met	Ser	Asp	Phe
		995				1000					1005				
Thr	Tyr	Val	Val	Glu	Asp	Met	Ala	Gly	Asn	Ile	Thr	Tyr	Thr	Pro	Val
	1010					1015					1020				
Thr	Lys	Leu	Leu	Glu	Gly	His	Ser	Asn	Lys	Pro	Glu	Gln	Asp	Gly	Ser
1025				1030					1035					1040	
Asp	Gln	Ala	Pro	Asp	Lys	Lys	Pro	Glu	Ala	Lys	Pro	Glu	Gln	Asp	Gly
			1045					1050						1055	
Ser	Gly	Gln	Thr	Pro	Asp	Lys	Lys	Lys	Glu	Thr	Lys	Pro	Glu	Lys	Asp
		1060					1065					1070			
Ser	Ser	Gly	Gln	Thr	Pro	Gly	Lys	Thr	Pro	Gln	Lys	Gly	Gln	Ser	Ser
		1075				1080					1085				
Arg	Thr	Leu	Glu	Lys	Arg	Ser	Ser	Lys	Arg	Ala	Leu	Ala	Thr	Lys	Ala
	1090					1095					1100				
Ser	Thr	Arg	Asp	Gln	Leu	Pro	Thr	Thr	Asn	Asp	Lys	Asp	Thr	Asn	Arg
1105				1110					1115					1120	
Leu	His	Leu	Leu	Lys	Leu	Val	Met	Thr	Thr	Phe	Phe	Leu	Gly		
			1125					1130							

<210> SEQ ID NO 28

<211> LENGTH: 1109

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 28

Gln	Ser	Asp	Ile	Lys	Ala	Asn	Thr	Val	Thr	Glu	Asp	Thr	Pro	Ala	Thr
1				5					10					15	

Glu	Gln	Ala	Val	Glu	Pro	Pro	Gln	Pro	Ile	Ala	Val	Ser	Glu	Glu	Ser
			20				25						30		

Arg	Ser	Ser	Lys	Glu	Thr	Lys	Thr	Ser	Gln	Thr	Pro	Ser	Asp	Val	Gly
	35						40					45			

Glu 50	Thr	Val	Ala	Asp	Asp	Ala 55	Asn	Asp	Leu	Ala	Pro 60	Gln	Ala	Pro	Ala
Lys 65	Thr	Ala	Asp	Thr	Pro 70	Ala	Thr	Ser	Lys	Ala 75	Thr	Ile	Arg	Asp	Leu 80
Asn	Asp	Pro	Ser	His 85	Val	Lys	Thr	Leu	Gln 90	Glu	Lys	Ala	Gly	Lys 95	Gly
Ala	Gly	Thr	Val 100	Val	Ala	Val	Ile	Asp 105	Ala	Gly	Phe	Asp	Lys 110	Asn	His
Glu	Ala	Trp 115	Arg	Leu	Thr	Asp	Lys 120	Thr	Lys	Ala	Arg	Tyr 125	Gln	Ser	Lys
Glu	Asn 130	Leu	Glu	Lys	Ala	Lys 135	Lys	Glu	His	Gly	Ile 140	Thr	Tyr	Gly	Glu
Trp 145	Val	Asn	Asp	Lys	Val 150	Ala	Tyr	Tyr	His	Asp 155	Tyr	Ser	Lys	Asp	Gly 160
Lys	Asn	Ala	Val	Asp 165	Gln	Glu	His	Gly	Thr 170	His	Val	Ser	Gly	Ile 175	Leu
Ser	Gly	Asn	Ala 180	Pro	Ser	Glu	Met	Lys 185	Glu	Pro	Tyr	Arg	Leu 190	Glu	Gly
Ala	Met	Pro 195	Glu	Ala	Gln	Leu	Leu 200	Leu	Met	Arg	Val	Glu 205	Ile	Val	Asn
Gly	Leu 210	Ala	Asp	Tyr	Ala	Arg 215	Asn	Tyr	Ala	Gln	Ala 220	Ile	Arg	Asp	Ala
Val 225	Asn	Leu	Gly	Ala	Lys 230	Val	Ile	Asn	Met	Ser 235	Phe	Gly	Asn	Ala	Ala 240
Leu	Ala	Tyr	Ala	Asn 245	Leu	Pro	Asp	Glu	Thr 250	Lys	Lys	Ala	Phe	Asp 255	Tyr
Ala	Lys	Ser	Lys 260	Gly	Val	Ser	Ile	Val 265	Thr	Ser	Ala	Gly	Asn 270	Asp	Ser
Ser	Phe 275	Gly	Gly	Lys	Pro	Arg	Leu 280	Pro	Leu	Ala	Asp	His 285	Pro	Asp	Tyr
Gly	Val 290	Val	Gly	Thr	Pro	Ala 295	Ala	Ala	Asp	Ser	Thr 300	Leu	Thr	Val	Ala
Ser 305	Tyr	Ser	Pro	Asp	Lys 310	Gln	Leu	Thr	Glu	Thr 315	Ala	Thr	Val	Lys	Thr 320
Asp	Asp	His	Gln 325	Asp	Lys	Glu	Met	Pro	Val 330	Ile	Ser	Thr	Asn	Arg 335	Phe
Glu	Pro	Asn	Lys 340	Ala	Tyr	Asp	Tyr	Ala 345	Tyr	Ala	Asn	Arg	Gly 350	Thr	Lys
Glu	Asp	Asp 355	Phe	Lys	Asp	Val	Glu 360	Gly	Lys	Ile	Ala	Leu 365	Ile	Glu	Arg
Gly	Asp 370	Ile	Asp	Phe	Lys	Asp 375	Lys	Ile	Ala	Asn	Ala 380	Lys	Lys	Ala	Gly
Ala 385	Val	Gly	Val	Leu	Ile 390	Tyr	Asp	Asn	Gln	Asp 395	Lys	Gly	Phe	Pro	Ile 400
Glu	Leu	Pro	Asn 405	Val	Asp	Gln	Met	Pro	Ala 410	Ala	Phe	Ile	Ser	Arg 415	Arg
Asp	Gly	Leu 420	Leu	Leu	Lys	Asp	Asn	Pro 425	Pro	Lys	Thr	Ile	Thr	Phe 430	Asn
Ala	Thr 435	Pro	Lys	Val	Leu	Pro	Thr 440	Ala	Ser	Gly	Thr	Lys 445	Leu	Ser	Arg
Phe 450	Ser	Ser	Trp	Gly	Leu	Thr 455	Ala	Asp	Gly	Asn	Ile 460	Lys	Pro	Asp	Ile
Ala	Ala	Pro	Gly	Gln	Asp	Ile	Leu	Ser	Ser	Val	Ala	Asn	Asn	Lys	Tyr

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465	470	475	480
Ala Lys Leu Ser Gly Thr Ser Met Ser Ala Pro Leu Val Ala Gly Ile			
	485	490	495
Met Gly Leu Leu Gln Lys Gln Tyr Glu Thr Gln Tyr Pro Asp Met Thr			
	500	505	510
Pro Ser Glu Arg Leu Asp Leu Ala Lys Lys Val Leu Met Ser Ser Ala			
	515	520	525
Thr Ala Leu Tyr Asp Glu Asp Glu Lys Ala Tyr Phe Ser Pro Arg Gln			
	530	535	540
Gln Gly Ala Gly Ala Val Asp Ala Lys Lys Ala Ser Ala Ala Thr Met			
545	550	555	560
Tyr Val Thr Asp Lys Asp Asn Thr Ser Ser Lys Val His Leu Asn Asn			
	565	570	575
Val Ser Asp Lys Phe Glu Val Thr Val Thr Val His Asn Lys Ser Asp			
	580	585	590
Lys Pro Gln Glu Leu Tyr Tyr Gln Val Thr Val Gln Thr Asp Lys Val			
	595	600	605
Asp Gly Lys His Phe Ala Leu Ala Pro Lys Ala Leu Tyr Glu Thr Ser			
	610	615	620
Trp Gln Lys Ile Thr Ile Pro Ala Asn Ser Ser Lys Gln Val Thr Val			
625	630	635	640
Pro Ile Asp Ala Ser Arg Phe Ser Lys Asp Leu Leu Ala Gln Met Lys			
	645	650	655
Asn Gly Tyr Phe Leu Glu Gly Phe Val Arg Phe Lys Gln Asp Pro Thr			
	660	665	670
Lys Glu Glu Leu Met Ser Ile Pro Tyr Ile Gly Phe Arg Gly Asp Phe			
	675	680	685
Gly Asn Leu Ser Ala Leu Glu Lys Pro Ile Tyr Asp Ser Lys Asp Gly			
	690	695	700
Ser Ser Tyr Tyr His Glu Ala Asn Ser Asp Ala Lys Asp Gln Leu Asp			
705	710	715	720
Gly Asp Gly Leu Gln Phe Tyr Ala Leu Lys Asn Asn Phe Thr Ala Leu			
	725	730	735
Thr Thr Glu Ser Asn Pro Trp Thr Ile Ile Lys Ala Val Lys Glu Gly			
	740	745	750
Val Glu Asn Ile Glu Asp Ile Glu Ser Ser Glu Ile Thr Glu Thr Ile			
	755	760	765
Phe Ala Gly Thr Phe Ala Lys Gln Asp Asp Asp Ser His Tyr Tyr Ile			
	770	775	780
His Arg His Ala Asn Gly Lys Pro Tyr Ala Ala Ile Ser Pro Asn Gly			
785	790	795	800
Asp Gly Asn Arg Asp Tyr Val Gln Phe Gln Gly Thr Phe Leu Arg Asn			
	805	810	815
Ala Lys Asn Leu Val Ala Glu Val Leu Asp Lys Glu Gly Asn Val Val			
	820	825	830
Trp Thr Ser Glu Val Thr Glu Gln Val Val Lys Asn Tyr Asn Asn Asp			
	835	840	845
Leu Ala Ser Thr Leu Gly Ser Thr Arg Phe Glu Lys Thr Arg Trp Asp			
	850	855	860
Gly Lys Asp Lys Asp Gly Lys Val Val Ala Asn Gly Thr Tyr Thr Tyr			
865	870	875	880
Arg Val Arg Tyr Thr Pro Ile Ser Ser Gly Ala Lys Glu Gln His Thr			
	885	890	895

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Asp Phe Asp Val Ile Val Asp Asn Thr Thr Pro Glu Val Ala Thr Ser
 900 905 910
 Ala Thr Phe Ser Thr Glu Asp Ser Arg Leu Thr Leu Ala Ser Lys Pro
 915 920 925
 Lys Thr Ser Gln Pro Val Tyr Arg Glu Arg Ile Ala Tyr Thr Tyr Met
 930 935 940
 Asp Glu Asp Leu Pro Thr Thr Glu Tyr Ile Ser Pro Asn Glu Asp Gly
 945 950 955 960
 Thr Phe Thr Leu Pro Glu Glu Ala Glu Thr Met Glu Gly Ala Thr Val
 965 970 975
 Pro Leu Lys Met Ser Asp Phe Thr Tyr Val Val Glu Asp Met Ala Gly
 980 985 990
 Asn Ile Thr Tyr Thr Pro Val Thr Lys Leu Leu Glu Gly His Ser Asn
 995 1000 1005
 Lys Pro Glu Gln Asp Gly Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu
 1010 1015 1020
 Ala Lys Pro Glu Gln Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Lys
 1025 1030 1035 1040
 Glu Thr Lys Pro Glu Lys Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr
 1045 1050 1055
 Pro Gln Lys Gly Gln Ser Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys
 1060 1065 1070
 Arg Ala Leu Ala Thr Lys Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr
 1075 1080 1085
 Asn Asp Lys Asp Thr Asn Arg Leu His Leu Leu Lys Leu Val Met Thr
 1090 1095 1100
 Thr Phe Phe Leu Gly
 1105

 <210> SEQ ID NO 29
 <211> LENGTH: 1103
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

 <400> SEQUENCE: 29

 Met Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 1 5 10 15
 Ile Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
 20 25 30
 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Pro Pro
 35 40 45
 Gln Pro Ile Ala Val Ser Glu Glu Ser Arg Ser Ser Lys Glu Thr Lys
 50 55 60
 Thr Ser Gln Thr Pro Ser Asp Val Gly Glu Thr Val Ala Asp Asp Ala
 65 70 75 80
 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
 85 90 95
 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser His Val Lys
 100 105 110
 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
 115 120 125
 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
 130 135 140
 Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asn Leu Glu Lys Ala Lys

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145	150	155	160
Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala			
	165	170	175
Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Asn Ala Val Asp Gln Glu			
	180	185	190
His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu			
	195	200	205
Met Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu			
	210	215	220
Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg			
	225	230	235
Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val			
	245	250	255
Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro			
	260	265	270
Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser			
	275	280	285
Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Pro Arg			
	290	295	300
Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala			
	305	310	315
Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln			
	325	330	335
Leu Thr Glu Thr Ala Thr Val Lys Thr Asp Asp His Gln Asp Lys Glu			
	340	345	350
Met Pro Val Ile Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp			
	355	360	365
Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val			
	370	375	380
Glu Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp			
	385	390	395
Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr			
	405	410	415
Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln			
	420	425	430
Met Pro Ala Ala Phe Ile Ser Arg Arg Asp Gly Leu Leu Leu Lys Asp			
	435	440	445
Asn Pro Pro Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro			
	450	455	460
Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr			
	465	470	475
Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile			
	485	490	495
Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser			
	500	505	510
Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln			
	515	520	525
Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu			
	530	535	540
Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp			
	545	550	555
Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp			
	565	570	575

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Ala Lys Lys	Ala Ser	Ala Ala	Thr Met	Tyr Val	Thr Asp	Lys Asp	Asn	
	580		585			590		
Thr Ser Ser	Lys Val	His Leu	Asn Asn	Val Ser	Asp Lys	Phe Glu	Val	
	595		600		605			
Thr Val Thr	Val His	Asn Lys	Ser Asp	Lys Pro	Gln Glu	Leu Tyr	Tyr	
	610		615		620			
Gln Val Thr	Val Gln	Thr Asp	Lys Val	Asp Gly	Lys His	Phe Ala	Leu	
	625		630		635		640	
Ala Pro Lys	Ala Leu	Tyr Glu	Thr Ser	Trp Gln	Lys Ile	Thr Ile	Pro	
	645			650		655		
Ala Asn Ser	Ser Lys	Gln Val	Thr Val	Pro Ile	Asp Ala	Ser Arg	Phe	
	660		665		670			
Ser Lys Asp	Leu Leu	Ala Gln	Met Lys	Asn Gly	Tyr Phe	Leu Glu	Gly	
	675		680		685			
Phe Val Arg	Phe Lys	Gln Asp	Pro Thr	Lys Glu	Glu Leu	Met Ser	Ile	
	690		695		700			
Pro Tyr Ile	Gly Phe	Arg Gly	Asp Phe	Gly Asn	Leu Ser	Ala Leu	Glu	
	705		710		715		720	
Lys Pro Ile	Tyr Asp	Ser Lys	Asp Gly	Ser Ser	Tyr Tyr	His Glu	Ala	
	725		730			735		
Asn Ser Asp	Ala Lys	Asp Gln	Leu Asp	Gly Asp	Gly Leu	Gln Phe	Tyr	
	740		745			750		
Ala Leu Lys	Asn Asn	Phe Thr	Ala Leu	Thr Thr	Glu Ser	Asn Pro	Trp	
	755		760		765			
Thr Ile Ile	Lys Ala	Val Lys	Glu Gly	Val Glu	Asn Ile	Glu Asp	Ile	
	770		775		780			
Glu Ser Ser	Glu Ile	Thr Glu	Thr Ile	Phe Ala	Gly Thr	Phe Ala	Lys	
	785		790		795		800	
Gln Asp Asp	Asp Ser	His Tyr	Tyr Tyr	Ile His	Arg His	Ala Asn	Gly Lys	
	805			810		815		
Pro Tyr Ala	Ala Ile	Ser Pro	Asn Gly	Asp Gly	Asn Arg	Asp Tyr	Val	
	820		825		830			
Gln Phe Gln	Gly Thr	Phe Leu	Arg Asn	Ala Lys	Asn Leu	Val Ala	Glu	
	835		840		845			
Val Leu Asp	Lys Glu	Gly Asn	Val Val	Trp Thr	Ser Glu	Val Thr	Glu	
	850		855		860			
Gln Val Val	Lys Asn	Tyr Asn	Asn Asp	Leu Ala	Ser Thr	Leu Gly	Ser	
	865		870		875		880	
Thr Arg Phe	Glu Lys	Thr Arg	Trp Asp	Gly Lys	Asp Lys	Asp Gly	Lys	
	885		890			895		
Val Val Ala	Asn Gly	Thr Tyr	Thr Tyr	Arg Val	Arg Tyr	Thr Pro	Ile	
	900		905			910		
Ser Ser Gly	Ala Lys	Glu Gln	His Thr	Asp Phe	Asp Val	Ile Val	Asp	
	915		920		925			
Asn Thr Thr	Pro Glu	Val Ala	Thr Ser	Ala Thr	Phe Ser	Thr Glu	Asp	
	930		935		940			
Ser Arg Leu	Thr Leu	Ala Ser	Lys Pro	Lys Thr	Ser Gln	Pro Val	Tyr	
	945		950		955		960	
Arg Glu Arg	Ile Ala	Tyr Thr	Tyr Met	Asp Glu	Asp Leu	Pro Thr	Thr	
	965		970			975		
Glu Tyr Ile	Ser Pro	Asn Glu	Asp Gly	Thr Phe	Thr Leu	Pro Glu	Glu	
	980		985			990		

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Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
 995 1000 1005
 Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
 1010 1015 1020
 Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
 1025 1030 1035 1040
 Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp Gly
 1045 1050 1055
 Ser Gly Gln Thr Pro Asp Lys Lys Lys Glu Thr Lys Pro Glu Lys Asp
 1060 1065 1070
 Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Ser Ser
 1075 1080 1085
 Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys
 1090 1095 1100

 <210> SEQ ID NO 30
 <211> LENGTH: 1078
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

 <400> SEQUENCE: 30
 Gln Ser Asp Ile Lys Ala Asn Thr Val Thr Glu Asp Thr Pro Ala Thr
 1 5 10 15
 Glu Gln Ala Val Glu Pro Pro Gln Pro Ile Ala Val Ser Glu Glu Ser
 20 25 30
 Arg Ser Ser Lys Glu Thr Lys Thr Ser Gln Thr Pro Ser Asp Val Gly
 35 40 45
 Glu Thr Val Ala Asp Asp Ala Asn Asp Leu Ala Pro Gln Ala Pro Ala
 50 55 60
 Lys Thr Ala Asp Thr Pro Ala Thr Ser Lys Ala Thr Ile Arg Asp Leu
 65 70 75 80
 Asn Asp Pro Ser His Val Lys Thr Leu Gln Glu Lys Ala Gly Lys Gly
 85 90 95
 Ala Gly Thr Val Val Ala Val Ile Asp Ala Gly Phe Asp Lys Asn His
 100 105 110
 Glu Ala Trp Arg Leu Thr Asp Lys Thr Lys Ala Arg Tyr Gln Ser Lys
 115 120 125
 Glu Asn Leu Glu Lys Ala Lys Lys Glu His Gly Ile Thr Tyr Gly Glu
 130 135 140
 Trp Val Asn Asp Lys Val Ala Tyr Tyr His Asp Tyr Ser Lys Asp Gly
 145 150 155 160
 Lys Asn Ala Val Asp Gln Glu His Gly Thr His Val Ser Gly Ile Leu
 165 170 175
 Ser Gly Asn Ala Pro Ser Glu Met Lys Glu Pro Tyr Arg Leu Glu Gly
 180 185 190
 Ala Met Pro Glu Ala Gln Leu Leu Leu Met Arg Val Glu Ile Val Asn
 195 200 205
 Gly Leu Ala Asp Tyr Ala Arg Asn Tyr Ala Gln Ala Ile Arg Asp Ala
 210 215 220
 Val Asn Leu Gly Ala Lys Val Ile Asn Met Ser Phe Gly Asn Ala Ala
 225 230 235 240
 Leu Ala Tyr Ala Asn Leu Pro Asp Glu Thr Lys Lys Ala Phe Asp Tyr
 245 250 255
 Ala Lys Ser Lys Gly Val Ser Ile Val Thr Ser Ala Gly Asn Asp Ser
 260 265 270

Ser 275	Phe 280	Gly 290	Gly 295	Lys 300	Pro 305	Arg 310	Leu 315	Pro 320	Leu 325	Ala 330	Asp 335	His 340	Pro 345	Asp 350	Tyr 355
Gly 290	Val 295	Val 300	Gly 305	Thr 310	Pro 315	Ala 320	Ala 325	Ala 330	Asp 335	Ser 340	Thr 345	Leu 350	Thr 355	Val 360	Ala 365
Ser 305	Tyr 310	Ser 315	Pro 320	Asp 325	Lys 330	Gln 335	Leu 340	Thr 345	Glu 350	Thr 355	Ala 360	Thr 365	Val 370	Lys 375	Thr 380
Asp 335	Asp 340	His 345	Gln 350	Asp 355	Lys 360	Glu 365	Met 370	Pro 375	Val 380	Ile 385	Ser 390	Thr 395	Asn 400	Arg 405	Phe 410
Glu 360	Pro 365	Asn 370	Lys 375	Ala 380	Tyr 385	Asp 390	Tyr 395	Ala 400	Tyr 405	Ala 410	Asn 415	Arg 420	Gly 425	Thr 430	Lys 435
Glu 385	Asp 390	Asp 395	Phe 400	Lys 405	Asp 410	Val 415	Glu 420	Gly 425	Lys 430	Ile 435	Ala 440	Leu 445	Ile 450	Glu 455	Arg 460
Gly 370	Asp 375	Ile 380	Asp 385	Phe 390	Lys 395	Asp 400	Lys 405	Ile 410	Ala 415	Asn 420	Ala 425	Lys 430	Lys 435	Ala 440	Gly 445
Ala 385	Val 390	Gly 395	Val 400	Leu 405	Ile 410	Tyr 415	Asp 420	Asn 425	Gln 430	Asp 435	Lys 440	Gly 445	Phe 450	Pro 455	Ile 460
Glu 410	Leu 415	Pro 420	Asn 425	Val 430	Asp 435	Gln 440	Met 445	Pro 450	Ala 455	Ala 460	Phe 465	Ile 470	Ser 475	Arg 480	Arg 485
Asp 435	Gly 440	Leu 445	Leu 450	Leu 455	Lys 460	Asp 465	Asn 470	Pro 475	Pro 480	Lys 485	Thr 490	Ile 495	Thr 500	Phe 505	Asn 510
Ala 460	Thr 465	Pro 470	Lys 475	Val 480	Leu 485	Pro 490	Thr 495	Ala 500	Ser 505	Gly 510	Thr 515	Lys 520	Leu 525	Ser 530	Arg 535
Phe 450	Ser 455	Ser 460	Trp 465	Gly 470	Leu 475	Thr 480	Ala 485	Asp 490	Gly 495	Asn 500	Ile 505	Lys 510	Pro 515	Asp 520	Ile 525
Ala 465	Ala 470	Pro 475	Gly 480	Gln 485	Asp 490	Ile 495	Leu 500	Ser 505	Ser 510	Val 515	Ala 520	Asn 525	Asn 530	Lys 535	Tyr 540
Ala 490	Lys 495	Leu 500	Ser 505	Gly 510	Thr 515	Ser 520	Met 525	Ser 530	Ala 535	Pro 540	Leu 545	Val 550	Ala 555	Gly 560	Ile 565
Met 515	Gly 520	Leu 525	Leu 530	Gln 535	Lys 540	Gln 545	Tyr 550	Glu 555	Thr 560	Gln 565	Tyr 570	Pro 575	Asp 580	Met 585	Thr 590
Pro 540	Ser 545	Glu 550	Arg 555	Leu 560	Asp 565	Leu 570	Ala 575	Lys 580	Lys 585	Val 590	Leu 595	Met 600	Ser 605	Ser 610	Ala 615
Thr 530	Ala 535	Leu 540	Tyr 545	Asp 550	Glu 555	Asp 560	Glu 565	Lys 570	Ala 575	Tyr 580	Phe 585	Ser 590	Pro 595	Arg 600	Gln 605
Gln 545	Gly 550	Ala 555	Gly 560	Ala 565	Val 570	Asp 575	Ala 580	Lys 585	Lys 590	Ala 595	Ser 600	Ala 605	Ala 610	Thr 615	Met 620
Tyr 570	Val 575	Thr 580	Asp 585	Lys 590	Asp 595	Asn 600	Thr 605	Ser 610	Ser 615	Lys 620	Val 625	His 630	Leu 635	Asn 640	Asn 645
Val 595	Ser 600	Asp 605	Lys 610	Phe 615	Glu 620	Val 625	Thr 630	Val 635	Thr 640	Val 645	His 650	Asn 655	Lys 660	Ser 665	Asp 670
Lys 620	Pro 625	Gln 630	Glu 635	Leu 640	Tyr 645	Tyr 650	Gln 655	Val 660	Thr 665	Val 670	Gln 675	Thr 680	Asp 685	Lys 690	Val 695
Asp 645	Gly 650	Lys 655	His 660	Phe 665	Ala 670	Leu 675	Ala 680	Pro 685	Lys 690	Ala 695	Leu 700	Tyr 705	Glu 710	Thr 715	Ser 720
Trp 625	Gln 630	Lys 635	Ile 640	Thr 645	Ile 650	Pro 655	Ala 660	Asn 665	Ser 670	Ser 675	Lys 680	Gln 685	Val 690	Thr 695	Val 700
Pro 655	Ile 660	Asp 665	Ala 670	Ser 675	Arg 680	Phe 685	Ser 690	Lys 695	Asp 700	Leu 705	Leu 710	Ala 715	Gln 720	Met 725	Lys 730
Asn 680	Gly 685	Tyr 690	Phe												

[illegible]

<210> SEQ ID NO 31
<211> LENGTH: 1365
<212> TYPE: DNA

-continued

<213> ORGANISM: *Streptococcus agalactiae*

<400> SEQUENCE: 31

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atgggacgag taatgaaaac aataacaaca ttgaaaata aaaaagtttt agtccttggt    60
ttagcacgat ctggagaagc tgctgcacgt ttgttagcta agttaggagc aatagtgaca    120
gttaatgatg gcaaaccatt tgatgaaaat ccaacagcac agtccttggt ggaagagggg    180
attaaagtgg ttgtggttag tcatccttta gaattgtag atgaggattt ttgttacatg    240
attaaaaatc caggaatacc ttataacaat cctatggtea aaaaagcatt agaaaaacaa    300
atccctgttt tgactgaagt ggaattagca tacttagttt cagaatctca gctaataagg    360
attacaggct ctaacgggaa aacgacaacg acaacgatga ttgcagaagt cttaaatgct    420
ggaggtcaga gaggtttggt agctgggaat atcggctttc ctgctagtga agttgttcag    480
gctgcgaatg ataaagatac tctagttagt gaattatcaa gttttcagct aatgggagtt    540
aaggaatttc gtctcatat tgacgaatg actaatgtaa tgccaactca tttagattat    600
catgggtctt ttgaagatta tggtgtgca aaatggaata tccaaactca aatgtcttca    660
tctgattttt tggactactaa ttttaataca ggtatttcta aagagtttag taaaactact    720
aaagcaacaa tcgttctctt ctctactacg gaaaaagtgt atggtgctta cgtacaagac    780
aagcaacttt tctataaagg ggagaatatt atgtcagtag atgacattgg tgtccagga    840
agccataacg tagagaatgc tctagcaact attgcggttg ctaaaactggc tggatatcag    900
aatcaagtta ttagagaaac tttaagcaat tttggaggtg ttaaacaccg cttgcaatca    960
ctcggttaagg ttcattggtat tagtttctat aacgacagca agtcaactaa tatattggca    1020
actcaaaaag cattatctgg ctttgataat actaaagtta tcctaattgc aggaggtctt    1080
gatcgcggtg atgagtttga tgaattgata ccagatatca ctggacttaa acatatgggt    1140
gttttagggg aatcggcatc tcgagtaaaa cgtgctgcac aaaaagcagg agtaacttat    1200
agcgatgctt tagatgtagt agatgcggtg cataaagctt atgaggtggc acaacagggc    1260
gatgttatct tgctaagtcc tgcaaatgca tcatgggaca tgtataagaa tttcgaagtc    1320
cgtggtgatg aattcattga tactttcgaa agtcttagag gagag                    1365

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<210> SEQ ID NO 32

<211> LENGTH: 455

<212> TYPE: PRT

<213> ORGANISM: *Streptococcus agalactiae*

<400> SEQUENCE: 32

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Met Gly Arg Val Met Lys Thr Ile Thr Thr Phe Glu Asn Lys Lys Val
  1           5           10           15
Leu Val Leu Gly Leu Ala Arg Ser Gly Glu Ala Ala Ala Arg Leu Leu
  20           25           30
Ala Lys Leu Gly Ala Ile Val Thr Val Asn Asp Gly Lys Pro Phe Asp
  35           40           45
Glu Asn Pro Thr Ala Gln Ser Leu Leu Glu Glu Gly Ile Lys Val Val
  50           55           60
Cys Gly Ser His Pro Leu Glu Leu Leu Asp Glu Asp Phe Cys Tyr Met
  65           70           75           80
Ile Lys Asn Pro Gly Ile Pro Tyr Asn Asn Pro Met Val Lys Lys Ala
  85           90           95
Leu Glu Lys Gln Ile Pro Val Leu Thr Glu Val Glu Leu Ala Tyr Leu
 100          105          110

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Thr	Val	Asn	Asp	Gly	Lys	Pro	Phe	Asp	Glu	Asn	Pro	Thr	Ala	Gln	Ser
	35						40					45			
Leu	Leu	Glu	Glu	Gly	Ile	Lys	Val	Val	Cys	Gly	Ser	His	Pro	Leu	Glu
	50					55					60				
Leu	Leu	Asp	Glu	Asp	Phe	Cys	Tyr	Met	Ile	Lys	Asn	Pro	Gly	Ile	Pro
	65				70					75					80
Tyr	Asn	Asn	Pro	Met	Val	Lys	Lys	Ala	Leu	Glu	Lys	Gln	Ile	Pro	Val
				85					90					95	
Leu	Thr	Glu	Val	Glu	Leu	Ala	Tyr	Leu	Val	Ser	Glu	Ser	Gln	Leu	Ile
			100					105					110		
Gly	Ile	Thr	Gly	Ser	Asn	Gly	Lys	Thr	Thr	Thr	Thr	Thr	Met	Ile	Ala
		115					120						125		
Glu	Val	Leu	Asn	Ala	Gly	Gly	Gln	Arg	Gly	Leu	Leu	Ala	Gly	Asn	Ile
	130					135					140				
Gly	Phe	Pro	Ala	Ser	Glu	Val	Val	Gln	Ala	Ala	Asn	Asp	Lys	Asp	Thr
	145				150					155					160
Leu	Val	Met	Glu	Leu	Ser	Ser	Phe	Gln	Leu	Met	Gly	Val	Lys	Glu	Phe
				165					170					175	
Arg	Pro	His	Ile	Ala	Val	Ile	Thr	Asn	Leu	Met	Pro	Thr	His	Leu	Asp
			180					185					190		
Tyr	His	Gly	Ser	Phe	Glu	Asp	Tyr	Val	Ala	Ala	Lys	Trp	Asn	Ile	Gln
		195					200					205			
Asn	Gln	Met	Ser	Ser	Ser	Asp	Phe	Leu	Val	Leu	Asn	Phe	Asn	Gln	Gly
	210					215					220				
Ile	Ser	Lys	Glu	Leu	Ala	Lys	Thr	Thr	Lys	Ala	Thr	Ile	Val	Pro	Phe
	225				230					235					240
Ser	Thr	Thr	Glu	Lys	Val	Asp	Gly	Ala	Tyr	Val	Gln	Asp	Lys	Gln	Leu
				245					250					255	
Phe	Tyr	Lys	Gly	Glu	Asn	Ile	Met	Ser	Val	Asp	Asp	Ile	Gly	Val	Pro
			260					265					270		
Gly	Ser	His	Asn	Val	Glu	Asn	Ala	Leu	Ala	Thr	Ile	Ala	Val	Ala	Lys
		275					280					285			
Leu	Ala	Gly	Ile	Ser	Asn	Gln	Val	Ile	Arg	Glu	Thr	Leu	Ser	Asn	Phe
	290					295					300				
Gly	Gly	Val	Lys	His	Arg	Leu	Gln	Ser	Leu	Gly	Lys	Val	His	Gly	Ile
	305				310					315					320
Ser	Phe	Tyr	Asn	Asp	Ser	Lys	Ser	Thr	Asn	Ile	Leu	Ala	Thr	Gln	Lys
			325						330					335	
Ala	Leu	Ser	Gly	Phe	Asp	Asn	Thr	Lys	Val	Ile	Leu	Ile	Ala	Gly	Gly
			340					345					350		
Leu	Asp	Arg	Gly	Asn	Glu	Phe	Asp	Glu	Leu	Ile	Pro	Asp	Ile	Thr	Gly
	355						360					365			
Leu	Lys	His	Met	Val	Val	Leu	Gly	Glu	Ser	Ala	Ser	Arg	Val	Lys	Arg
	370					375					380				
Ala	Ala	Gln	Lys	Ala	Gly	Val	Thr	Tyr	Ser	Asp	Ala	Leu	Asp	Val	Arg
	385				390					395					400
Asp	Ala	Val	His	Lys	Ala	Tyr	Glu	Val	Ala	Gln	Gln	Gly	Asp	Val	Ile
				405					410					415	
Leu	Leu	Ser	Pro	Ala	Asn	Ala	Ser	Trp	Asp	Met	Tyr	Lys	Asn	Phe	Glu
			420					425					430		
Val	Arg	Gly	Asp	Glu	Phe	Ile	Asp	Thr	Phe	Glu	Ser	Leu	Arg	Gly	Glu
		435					440						445		

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<210> SEQ ID NO 34
<211> LENGTH: 334
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 34
Met Gly Arg Val Met Lys Thr Ile Thr Thr Phe Glu Asn Lys Lys Val
 1         5         10         15
Leu Val Leu Gly Leu Ala Arg Ser Gly Glu Ala Ala Ala Arg Leu Leu
 20        25        30
Ala Lys Leu Gly Ala Ile Val Thr Val Asn Asp Gly Lys Pro Phe Asp
 35        40        45
Glu Asn Pro Thr Ala Gln Ser Leu Leu Glu Glu Gly Ile Lys Val Val
 50        55        60
Cys Gly Ser His Pro Leu Glu Leu Leu Asp Glu Asp Phe Cys Tyr Met
 65        70        75        80
Ile Lys Asn Pro Gly Ile Pro Tyr Asn Asn Pro Met Val Lys Lys Ala
 85        90        95
Leu Glu Lys Gln Ile Pro Val Leu Thr Glu Val Glu Leu Ala Tyr Leu
100       105       110
Val Ser Glu Ser Gln Leu Ile Gly Ile Thr Gly Ser Asn Gly Lys Thr
115       120       125
Thr Thr Thr Thr Met Ile Ala Glu Val Leu Asn Ala Gly Gly Gln Arg
130       135       140
Gly Leu Leu Ala Gly Asn Ile Gly Phe Pro Ala Ser Glu Val Val Gln
145       150       155       160
Ala Ala Asn Asp Lys Asp Thr Leu Val Met Glu Leu Ser Ser Phe Gln
165       170       175
Leu Met Gly Val Lys Glu Phe Arg Pro His Ile Ala Val Ile Thr Asn
180       185       190
Leu Met Pro Thr His Leu Asp Tyr His Gly Ser Phe Glu Asp Tyr Val
195       200       205
Ala Ala Lys Trp Asn Ile Gln Asn Gln Met Ser Ser Ser Asp Phe Leu
210       215       220
Val Leu Asn Phe Asn Gln Gly Ile Ser Lys Glu Leu Ala Lys Thr Thr
225       230       235       240
Lys Ala Thr Ile Val Pro Phe Ser Thr Thr Glu Lys Val Asp Gly Ala
245       250       255
Tyr Val Gln Asp Lys Gln Leu Phe Tyr Lys Gly Glu Asn Ile Met Ser
260       265       270
Val Asp Asp Ile Gly Val Pro Gly Ser His Asn Val Glu Asn Ala Leu
275       280       285
Ala Thr Ile Ala Val Ala Lys Leu Ala Gly Ile Ser Asn Gln Val Ile
290       295       300
Arg Glu Thr Leu Ser Asn Phe Gly Gly Val Lys His Arg Leu Gln Ser
305       310       315       320
Leu Gly Lys Val His Gly Ile Ser Phe Tyr Asn Asp Ser Lys
325       330

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<210> SEQ ID NO 35
<211> LENGTH: 327
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 35

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Ile 1	Thr	Thr	Phe	Glu 5	Asn	Lys	Lys	Val	Leu 10	Val	Leu	Gly	Leu	Ala 15	Arg
Ser	Gly	Glu	Ala 20	Ala	Ala	Arg	Leu	Leu 25	Ala	Lys	Leu	Gly	Ala 30	Ile	Val
Thr	Val	Asn 35	Asp	Gly	Lys	Pro	Phe 40	Asp	Glu	Asn	Pro	Thr 45	Ala	Gln	Ser
Leu 50	Leu	Glu	Glu	Gly	Ile 55	Lys	Val	Val	Cys	Gly	Ser 60	His	Pro	Leu	Glu
Leu 65	Leu	Asp	Glu	Asp	Phe 70	Cys	Tyr	Met	Ile	Lys 75	Asn	Pro	Gly	Ile	Pro 80
Tyr	Asn	Asn	Pro	Met 85	Val	Lys	Lys	Ala 90	Leu	Glu	Lys	Gln	Ile	Pro 95	Val
Leu	Thr	Glu	Val 100	Glu	Leu	Ala	Tyr	Leu 105	Val	Ser	Glu	Ser	Gln 110	Leu	Ile
Gly	Ile	Thr 115	Gly	Ser	Asn	Gly	Lys 120	Thr	Thr	Thr	Thr	Thr 125	Met	Ile	Ala
Glu 130	Val	Leu	Asn	Ala	Gly	Gly 135	Gln	Arg	Gly	Leu 140	Leu	Ala	Gly	Asn	Ile
Gly 145	Phe	Pro	Ala	Ser	Glu 150	Val	Val	Gln	Ala	Ala 155	Asn	Asp	Lys	Asp	Thr 160
Leu	Val	Met	Glu	Leu 165	Ser	Ser	Phe	Gln	Leu 170	Met	Gly	Val	Lys	Glu	Phe 175
Arg	Pro	His	Ile 180	Ala	Val	Ile	Thr	Asn 185	Leu	Met	Pro	Thr 190	His	Leu	Asp
Tyr	His	Gly 195	Ser	Phe	Glu	Asp	Tyr 200	Val	Ala	Ala	Lys	Trp 205	Asn	Ile	Gln
Asn 210	Gln	Met	Ser	Ser	Ser	Asp 215	Phe	Leu	Val	Leu	Asn 220	Phe	Asn	Gln	Gly
Ile 225	Ser	Lys	Glu	Leu	Ala 230	Lys	Thr	Thr	Lys	Ala 235	Thr	Ile	Val	Pro	Phe 240
Ser	Thr	Thr	Glu	Lys 245	Val	Asp	Gly	Ala	Tyr 250	Val	Gln	Asp	Lys	Gln	Leu
Phe	Tyr	Lys	Gly 260	Glu	Asn	Ile	Met	Ser 265	Val	Asp	Asp	Ile	Gly 270	Val	Pro
Gly	Ser	His 275	Asn	Val	Glu	Asn	Ala 280	Leu	Ala	Thr	Ile	Ala 285	Val	Ala	Lys
Leu 290	Ala	Gly	Ile	Ser	Asn	Gln	Val 295	Ile	Arg	Glu	Thr 300	Leu	Ser	Asn	Phe
Gly 305	Gly	Val	Lys	His 310	Arg	Leu	Gln	Ser	Leu	Gly 315	Lys	Val	His	Gly	Ile 320
Ser	Phe	Tyr	Asn 325	Asp	Ser	Lys									

<400> SEQUENCE: 36

atgaataaaa aggtactatt gacatcgaca atggcagctt cgctattatc agtcgcaagt	60
gttcaagcac aagaaacaga tacgacgtgg acagcacgta ctgtttcaga ggtaaaggct	120
gatttggtaa agcaagacaa taaatcatca tatactgtga aatatggtga tacactaagc	180
gttatttcag aagcaatgtc aattgatatg aatgtcttag caaaaataaa taacattgca	240

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gatatcaatc ttatttatcc tgagacaaca ctgacagtaa cttacgatca gaagagtcac 300
actgccactt caatgaaaat agaaacacca gcaacaaatg ctgctgggtca aacaacagct 360
actgtggatt tgaaaaccaa tcaagtttct gttgcagacc aaaaagtttc tctcaataca 420
atttcggaag gtatgacacc agaagcagca acaacgattg tttcgccaat gaagacatat 480
tcttctgcgc cagctttgaa atcaaaagaa gtattagcac aagagcaagc tgttagtcaa 540
gcagcagcta atgaacaggt atcaccagct cctgtgaagt cgattacttc agaagttcca 600
gcagctaaag aggaagttaa accaactcag acgtcagtcg gtcagtcaac aacagtatca 660
ccagcttctg ttgccgctga aacaccagct ccagtagcta aagtagcacc ggtaagaact 720
gtagcagccc ctagagtggc aagtgttaaa gtagtcactc ctaaagtaga aactgggtgca 780
tcaccagagc atgtatcagc tccagcagtt cctgtgacta cgacttcacc agctacagac 840
agtaagttac aagcgactga agttaagagc gttccggtag cacaaaaagc tccaacagca 900
acaccggtag cacaaccagc ttcaacaaca aatgcagtag ctgcacatcc tgaatatgca 960
ggggtccaac ctcatgttgc agcttataaa gaaaaagtag cgtcaactta tggagttaat 1020
gaattcagta catacctgac gggagatcca ggtgatcatg gtaaaagttt agcagttgac 1080
tttattgtag gtactaatca agcacttggt aataaagttg cacagtactc tacacaaaat 1140
atggcagcaa ataacatttc atatgttatac tggcaacaaa agttttactc aaatacaaac 1200
agtatttatg gacctgctaa tacttggaat gcaatgccag atcgtggtgg cgttactgcc 1260
aaccactatg accacgttca cgtatcattt aacaaataat ataaaaaagg aagctatttg 1320
gcttcttttt tatatgcctt gaatagactt tcaaggttct tatataattt ttatta 1376

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<210> SEQ ID NO 37

<211> LENGTH: 432

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 37

```

Met Asn Lys Lys Val Leu Leu Thr Ser Thr Met Ala Ala Ser Leu Leu
 1             5             10             15

Ser Val Ala Ser Val Gln Ala Gln Glu Thr Asp Thr Thr Trp Thr Ala
 20             25             30

Arg Thr Val Ser Glu Val Lys Ala Asp Leu Val Lys Gln Asp Asn Lys
 35             40             45

Ser Ser Tyr Thr Val Lys Tyr Gly Asp Thr Leu Ser Val Ile Ser Glu
 50             55             60

Ala Met Ser Ile Asp Met Asn Val Leu Ala Lys Ile Asn Asn Ile Ala
 65             70             75             80

Asp Ile Asn Leu Ile Tyr Pro Glu Thr Thr Leu Thr Val Thr Tyr Asp
 85             90             95

Gln Lys Ser His Thr Ala Thr Ser Met Lys Ile Glu Thr Pro Ala Thr
100             105             110

Asn Ala Ala Gly Gln Thr Thr Ala Thr Val Asp Leu Lys Thr Asn Gln
115             120             125

Val Ser Val Ala Asp Gln Lys Val Ser Leu Asn Thr Ile Ser Glu Gly
130             135             140

Met Thr Pro Glu Ala Ala Thr Thr Ile Val Ser Pro Met Lys Thr Tyr
145             150             155             160

Ser Ser Ala Pro Ala Leu Lys Ser Lys Glu Val Leu Ala Gln Glu Gln
165             170             175

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Ala	Val	Ser	Gln	Ala	Ala	Ala	Asn	Glu	Gln	Val	Ser	Pro	Ala	Pro	Val
			180					185					190		
Lys	Ser	Ile	Thr	Ser	Glu	Val	Pro	Ala	Ala	Lys	Glu	Glu	Val	Lys	Pro
	195						200					205			
Thr	Gln	Thr	Ser	Val	Ser	Gln	Ser	Thr	Thr	Val	Ser	Pro	Ala	Ser	Val
	210					215					220				
Ala	Ala	Glu	Thr	Pro	Ala	Pro	Val	Ala	Lys	Val	Ala	Pro	Val	Arg	Thr
225					230					235					240
Val	Ala	Ala	Pro	Arg	Val	Ala	Ser	Val	Lys	Val	Val	Thr	Pro	Lys	Val
			245						250					255	
Glu	Thr	Gly	Ala	Ser	Pro	Glu	His	Val	Ser	Ala	Pro	Ala	Val	Pro	Val
		260						265					270		
Thr	Thr	Thr	Ser	Pro	Ala	Thr	Asp	Ser	Lys	Leu	Gln	Ala	Thr	Glu	Val
		275					280					285			
Lys	Ser	Val	Pro	Val	Ala	Gln	Lys	Ala	Pro	Thr	Ala	Thr	Pro	Val	Ala
	290					295					300				
Gln	Pro	Ala	Ser	Thr	Thr	Asn	Ala	Val	Ala	Ala	His	Pro	Glu	Asn	Ala
305					310					315					320
Gly	Leu	Gln	Pro	His	Val	Ala	Ala	Tyr	Lys	Glu	Lys	Val	Ala	Ser	Thr
			325						330					335	
Tyr	Gly	Val	Asn	Glu	Phe	Ser	Thr	Tyr	Arg	Ala	Gly	Asp	Pro	Gly	Asp
		340						345					350		
His	Gly	Lys	Gly	Leu	Ala	Val	Asp	Phe	Ile	Val	Gly	Thr	Asn	Gln	Ala
		355					360					365			
Leu	Gly	Asn	Lys	Val	Ala	Gln	Tyr	Ser	Thr	Gln	Asn	Met	Ala	Ala	Asn
	370					375					380				
Asn	Ile	Ser	Tyr	Val	Ile	Trp	Gln	Gln	Lys	Phe	Tyr	Ser	Asn	Thr	Asn
385					390					395					400
Ser	Ile	Tyr	Gly	Pro	Ala	Asn	Thr	Trp	Asn	Ala	Met	Pro	Asp	Arg	Gly
			405						410					415	
Gly	Val	Thr	Ala	Asn	His	Tyr	Asp	His	Val	His	Val	Ser	Phe	Asn	Lys
		420						425					430		

<210> SEQ ID NO 38

<211> LENGTH: 392

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 38

Asp	Leu	Val	Lys	Gln	Asp	Asn	Lys	Ser	Ser	Tyr	Thr	Val	Lys	Tyr	Gly
1			5					10					15		
Asp	Thr	Leu	Ser	Val	Ile	Ser	Glu	Ala	Met	Ser	Ile	Asp	Met	Asn	Val
	20						25					30			
Leu	Ala	Lys	Ile	Asn	Asn	Ile	Ala	Asp	Ile	Asn	Leu	Ile	Tyr	Pro	Glu
	35					40					45				
Thr	Thr	Leu	Thr	Val	Thr	Tyr	Asp	Gln	Lys	Ser	His	Thr	Ala	Thr	Ser
	50					55					60				
Met	Lys	Ile	Glu	Thr	Pro	Ala	Thr	Asn	Ala	Ala	Gly	Gln	Thr	Thr	Ala
65					70					75					80
Thr	Val	Asp	Leu	Lys	Thr	Asn	Gln	Val	Ser	Val	Ala	Asp	Gln	Lys	Val
			85						90					95	
Ser	Leu	Asn	Thr	Ile	Ser	Glu	Gly	Met	Thr	Pro	Glu	Ala	Ala	Thr	Thr
		100						105					110		
Ile	Val	Ser	Pro	Met	Lys	Thr	Tyr	Ser	Ser	Ala	Pro	Ala	Leu	Lys	Ser
		115						120					125		

-continued

Lys Glu Val Leu Ala Gln Glu Gln Ala Val Ser Gln Ala Ala Ala Asn
 130 135 140
 Glu Gln Val Ser Pro Ala Pro Val Lys Ser Ile Thr Ser Glu Val Pro
 145 150 155 160
 Ala Ala Lys Glu Glu Val Lys Pro Thr Gln Thr Ser Val Ser Gln Ser
 165 170 175
 Thr Thr Val Ser Pro Ala Ser Val Ala Ala Glu Thr Pro Ala Pro Val
 180 185 190
 Ala Lys Val Ala Pro Val Arg Thr Val Ala Ala Pro Arg Val Ala Ser
 195 200 205
 Val Lys Val Val Thr Pro Lys Val Glu Thr Gly Ala Ser Pro Glu His
 210 215 220
 Val Ser Ala Pro Ala Val Pro Val Thr Thr Thr Ser Pro Ala Thr Asp
 225 230 235 240
 Ser Lys Leu Gln Ala Thr Glu Val Lys Ser Val Pro Val Ala Gln Lys
 245 250 255
 Ala Pro Thr Ala Thr Pro Val Ala Gln Pro Ala Ser Thr Thr Asn Ala
 260 265 270
 Val Ala Ala His Pro Glu Asn Ala Gly Leu Gln Pro His Val Ala Ala
 275 280 285
 Tyr Lys Glu Lys Val Ala Ser Thr Tyr Gly Val Asn Glu Phe Ser Thr
 290 295 300
 Tyr Arg Ala Gly Asp Pro Gly Asp His Gly Lys Gly Leu Ala Val Asp
 305 310 315 320
 Phe Ile Val Gly Thr Asn Gln Ala Leu Gly Asn Lys Val Ala Gln Tyr
 325 330 335
 Ser Thr Gln Asn Met Ala Ala Asn Asn Ile Ser Tyr Val Ile Trp Gln
 340 345 350
 Gln Lys Phe Tyr Ser Asn Thr Asn Ser Ile Tyr Gly Pro Ala Asn Thr
 355 360 365
 Trp Asn Ala Met Pro Asp Arg Gly Gly Val Thr Ala Asn His Tyr Asp
 370 375 380
 His Val His Val Ser Phe Asn Lys
 385 390

<210> SEQ ID NO 39

<211> LENGTH: 1500

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 39

```

atgaataaac gcgtaaaaat cgttgcaaca cttggtcctg cggttgaatt ccgtggtggt    60
aagaagtttg gtgagtctgg atactggggt gaaagccttg acgtagaagc ttcagcagaa    120
aaaattgctc aattgattaa agaaggtgct aacgttttcc gtttcaactt ctcacatgga    180
gatcatgctg agcaaggagc tcgtatggct actgttcgta aagcagaaga gattgcagga    240
caaaaagttg gtttcctcct tgatactaaa ggacctgaaa ttcgtacaga actttttgaa    300
gatgggtgcag atttccattc atatacaaca ggtacaaaat tacgtgttgc tactaagcaa    360
ggatatcaat caactccaga agtgattgca ttgaatgttg ctggtggact tgacatcttt    420
gatgacgttg aagttggtaa gcaaactcct gttgatgatg gtaaactagg tcttactgtg    480
tttgcaaaag ataaagacac tcgtgaattt gaagtagttg ttgagaatga tggccttatt    540
ggtaaacaaa aaggtgtaaa catcccttat actaaaattc ctttccagc acttcagaaa    600

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cgcgataatg ctgatatccg ttttggactt gagcaaggac ttaactttat tgctatctca    660
ttgttacgta ctgctaaaga tgtaaatgaa gttcgtgcta tttgtgaaga aactggsmat    720
ggacacggtta agttgtttgc taaaattgaa aatcaacaag gtatcgataa tattgatgag    780
attatcgaag cagcagatgg tattatgatt gtcgtggtg atatgggtat cgaagttcca    840
tttgaaatgg ttccagttta ccaaaaaatg atcattacta aagttaatgc agctggtaaa    900
gcagttatta cagcaacaaa tatgcttgaa acaatgactg ataaccacg tgcgactcgt    960
tcagaagtat ctgatgtctt caatgctgtt attgatggta ctgatgctac aatgctttca   1020
ggtgagtcag ctaatggtaa ataccagtt gagtcagttc gtacaatggc tactattgat   1080
aaaaatgctc aaacattact caatgagtat ggtcgcttag actcatctgc attccacgt    1140
aataacaaaa ctgatgttat tgcctctgcg gttaaagatg caacacactc aatggatate   1200
aaacttgttg taacaattac tgaacacaggt aatacagctc gtgccatttc taaattccgt   1260
ccagatgcag acattttggc tgttacattt gatgaaaaag tacaacgttc attgatgatt   1320
aactggggtg ttatccctgt ccttgcagac aaaccagcat ctacagatga tatgtttgag   1380
gttgcagaac gtgtagcact tgaagcagga tttgttgaat caggcgataa tatcgttatc   1440
gttcgaggtg ttcctgtagg tacaggtgga actaacacaa tgcgtgttcg tactgttaaa   1500

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<210> SEQ ID NO 40
<211> LENGTH: 500
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae
<220> FEATURE:
<221> NAME/KEY: VARIANT
<222> LOCATION: (1)...(500)
<223> OTHER INFORMATION: Xaa = Any Amino Acid

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<400> SEQUENCE: 40

```

```

Met Asn Lys Arg Val Lys Ile Val Ala Thr Leu Gly Pro Ala Val Glu
 1             5             10            15
Phe Arg Gly Gly Lys Lys Phe Gly Glu Ser Gly Tyr Trp Gly Glu Ser
          20            25            30
Leu Asp Val Glu Ala Ser Ala Glu Lys Ile Ala Gln Leu Ile Lys Glu
          35            40            45
Gly Ala Asn Val Phe Arg Phe Asn Phe Ser His Gly Asp His Ala Glu
          50            55            60
Gln Gly Ala Arg Met Ala Thr Val Arg Lys Ala Glu Glu Ile Ala Gly
          65            70            75            80
Gln Lys Val Gly Phe Leu Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr
          85            90            95
Glu Leu Phe Glu Asp Gly Ala Asp Phe His Ser Tyr Thr Thr Gly Thr
          100           105           110
Lys Leu Arg Val Ala Thr Lys Gln Gly Ile Lys Ser Thr Pro Glu Val
          115           120           125
Ile Ala Leu Asn Val Ala Gly Gly Leu Asp Ile Phe Asp Asp Val Glu
          130           135           140
Val Gly Lys Gln Ile Leu Val Asp Asp Gly Lys Leu Gly Leu Thr Val
          145           150           155           160
Phe Ala Lys Asp Lys Asp Thr Arg Glu Phe Glu Val Val Val Glu Asn
          165           170           175
Asp Gly Leu Ile Gly Lys Gln Lys Gly Val Asn Ile Pro Tyr Thr Lys
          180           185           190

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Ile Pro Phe Pro Ala Leu Ala Glu Arg Asp Asn Ala Asp Ile Arg Phe
195 200 205

Gly Leu Glu Gln Gly Leu Asn Phe Ile Ala Ile Ser Phe Val Arg Thr
210 215 220

Ala Lys Asp Val Asn Glu Val Arg Ala Ile Cys Glu Glu Thr Gly Xaa
225 230 235 240

Gly His Val Lys Leu Phe Ala Lys Ile Glu Asn Gln Gln Gly Ile Asp
245 250 255

Asn Ile Asp Glu Ile Ile Glu Ala Ala Asp Gly Ile Met Ile Ala Arg
260 265 270

Gly Asp Met Gly Ile Glu Val Pro Phe Glu Met Val Pro Val Tyr Gln
275 280 285

Lys Met Ile Ile Thr Lys Val Asn Ala Ala Gly Lys Ala Val Ile Thr
290 295 300

Ala Thr Asn Met Leu Glu Thr Met Thr Asp Lys Pro Arg Ala Thr Arg
305 310 315 320

Ser Glu Val Ser Asp Val Phe Asn Ala Val Ile Asp Gly Thr Asp Ala
325 330 335

Thr Met Leu Ser Gly Glu Ser Ala Asn Gly Lys Tyr Pro Val Glu Ser
340 345 350

Val Arg Thr Met Ala Thr Ile Asp Lys Asn Ala Gln Thr Leu Leu Asn
355 360 365

Glu Tyr Gly Arg Leu Asp Ser Ser Ala Phe Pro Arg Asn Asn Lys Thr
370 375 380

Asp Val Ile Ala Ser Ala Val Lys Asp Ala Thr His Ser Met Asp Ile
385 390 395 400

Lys Leu Val Val Thr Ile Thr Glu Thr Gly Asn Thr Ala Arg Ala Ile
405 410 415

Ser Lys Phe Arg Pro Asp Ala Asp Ile Leu Ala Val Thr Phe Asp Glu
420 425 430

Lys Val Gln Arg Ser Leu Met Ile Asn Trp Gly Val Ile Pro Val Leu
435 440 445

Ala Asp Lys Pro Ala Ser Thr Asp Asp Met Phe Glu Val Ala Glu Arg
450 455 460

Val Ala Leu Glu Ala Gly Phe Val Glu Ser Gly Asp Asn Ile Val Ile
465 470 475 480

Val Ala Gly Val Pro Val Gly Thr Gly Gly Thr Asn Thr Met Arg Val
485 490 495

Arg Thr Val Lys
500

<210> SEQ ID NO 41
 <211> LENGTH: 720
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 41

ttgtctgcta taatagacaa aaagtggtg atatttatgt atttagcatt aatcggtgat	60
atcattaatt caaaacagat acttgaacgt gaaactttcc aacagtcttt tcagcaacta	120
atgaccgaac tatctgatgt atatggtgaa gagctgattt ctccattcac tattacagct	180
ggtgatgaat ttcaagcttt attgaaacca tcaaaaaagg tatttcaaatt tattgaccat	240
attcaactag ctctaaaacc tgtaaatgta aggttcggcc tcggtacagg aaacattata	300
acatccatca attcaaatga aagtatcggg gctgatgggc ctgcctactg gcatgctcgc	360

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tcagctatta atcatatata tgataaaaat gattatggaa cagttcaagt agctatttgc 420
cttgatgatg aagacaaaaa ccttgaatta aactaaata gtctcatttc agctgggtgat 480
tttatcaagt caaaatggac tacaaacat tttcaaatgc ttgagcactt aataacttaa 540
gataattatc aagaacaatt tcaacatcaa aagttagccc aactggaaaa tattgaacct 600
agtgcgctga ctaaagcct taaagcaagc ggtctgaaga ttactttaag aacgagaaca 660
caggcagccg atctattagt taaaagttgc actcaaaacta aagggggaag ctatgatttc 720

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<210> SEQ ID NO 42
<211> LENGTH: 240
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 42

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```

Met Ser Ala Ile Ile Asp Lys Lys Val Val Ile Phe Met Tyr Leu Ala
 1             5             10            15
Leu Ile Gly Asp Ile Ile Asn Ser Lys Gln Ile Leu Glu Arg Glu Thr
      20             25            30
Phe Gln Gln Ser Phe Gln Gln Leu Met Thr Glu Leu Ser Asp Val Tyr
      35             40            45
Gly Glu Glu Leu Ile Ser Pro Phe Thr Ile Thr Ala Gly Asp Glu Phe
      50             55            60
Gln Ala Leu Leu Lys Pro Ser Lys Lys Val Phe Gln Ile Ile Asp His
      65             70            75            80
Ile Gln Leu Ala Leu Lys Pro Val Asn Val Arg Phe Gly Leu Gly Thr
      85             90            95
Gly Asn Ile Ile Thr Ser Ile Asn Ser Asn Glu Ser Ile Gly Ala Asp
      100            105           110
Gly Pro Ala Tyr Trp His Ala Arg Ser Ala Ile Asn His Ile His Asp
      115            120           125
Lys Asn Asp Tyr Gly Thr Val Gln Val Ala Ile Cys Leu Asp Asp Glu
      130            135           140
Asp Gln Asn Leu Glu Leu Thr Leu Asn Ser Leu Ile Ser Ala Gly Asp
      145            150           155           160
Phe Ile Lys Ser Lys Trp Thr Thr Asn His Phe Gln Met Leu Glu His
      165            170           175
Leu Ile Leu Gln Asp Asn Tyr Gln Glu Gln Phe Gln His Gln Lys Leu
      180            185           190
Ala Gln Leu Glu Asn Ile Glu Pro Ser Ala Leu Thr Lys Arg Leu Lys
      195            200           205
Ala Ser Gly Leu Lys Ile Tyr Leu Arg Thr Arg Thr Gln Ala Ala Asp
      210            215           220
Leu Leu Val Lys Ser Cys Thr Gln Thr Lys Gly Gly Ser Tyr Asp Phe
      225            230           235           240

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<210> SEQ ID NO 43
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 43

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```

Met Tyr Leu Ala Leu Ile Gly Asp Ile Ile Asn Ser Lys Gln Ile Leu
 1             5             10            15
Glu Arg Glu Thr Phe Gln Gln Ser Phe Gln Gln Leu Met Thr Glu Leu
      20             25            30

```

-continued

Ser Asp Val Tyr Gly Glu Glu Leu Ile Ser Pro Phe Thr Ile Thr Ala
35 40 45

Gly Asp Glu Phe Gln Ala Leu Leu Lys Pro Ser Lys Lys Val Phe Gln
50 55 60

Ile Ile Asp His Ile Gln Leu Ala Leu Lys Pro Val Asn Val Arg Phe
65 70 75 80

Gly Leu Gly Thr Gly Asn Ile Ile Thr Ser Ile Asn Ser Asn Glu Ser
85 90 95

Ile Gly Ala Asp Gly Pro Ala Tyr Trp His Ala Arg Ser Ala Ile Asn
100 105 110

His Ile His Asp Lys Asn Asp Tyr Gly Thr Val Gln Val Ala Ile Cys
115 120 125

Leu Asp Asp Glu Asp Gln Asn Leu Glu Leu Thr Leu Asn Ser Leu Ile
130 135 140

Ser Ala Gly Asp Phe Ile Lys Ser Lys Trp Thr Thr Asn His Phe Gln
145 150 155 160

Met Leu Glu His Leu Ile Leu Gln Asp Asn Tyr Gln Glu Gln Phe Gln
165 170 175

His Gln Lys Leu Ala Gln Leu Glu Asn Ile Glu Pro Ser Ala Leu Thr
180 185 190

Lys Arg Leu Lys Ala Ser Gly Leu Lys Ile Tyr Leu Arg Thr Arg Thr
195 200 205

Gln Ala Ala Asp Leu Leu Val Lys Ser Cys Thr Gln Thr Lys Gly Gly
210 215 220

Ser Tyr Asp Phe
225

<210> SEQ ID NO 44

<211> LENGTH: 2193

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 44

atgagcgtat atgttagtgg aataggaatt atttcttctt tgggaaagaa ttatagcgag 60

cataaacagc atctcttcga cttaaagaa ggaatttcta aacatttata taaaaatcac 120

gactctattt tagaatctta tacaggaagc ataactagt acccagaggt tctgagcaa 180

tacaaagatg agacacgtaa ttttaaattt gcttttaccg cttttgaaga ggctcttgct 240

tcttcaggtg ttaatttaaa agcttatcat aatattgctg tgtgtttagg gacctcactt 300

gggggaaaga gtgctggtca aaatgccttg tatcaatttg aagaaggaga gcgtcaagta 360

gatgctagtt tattagaaaa agcatctgtt taccatattg ctgatgaatt gatggcttat 420

catgatattg tgggagcttc gtatgttatt tcaaccgcct gttctgcaag taataatgcc 480

gtaatattag gaacacaatt acttcaagat ggcgattgtg atttagctat ttgtggtggc 540

tgtgatgagt taagtgatat ttcttttagca ggcttcacat cactaggagc tattaatata 600

gaaatggcat gtcagcccta ttcttctgga aaaggaatca atttgggtga ggcgctggt 660

tttgtgtgtc ttgtcaaaga tcagtcctta gctaaatatg gaaaaattat cgggtggtctt 720

attacttcag atgggttatca tataacagca cctaagccaa caggtgaagg ggcggcacag 780

attgcaaagc agctagtgc tcaagcaggt attgactaca gtgagattga ctatattaac 840

ggtcacggta caggtactca agctaagat aaaatggaaa aaaatatgta tggttaagttt 900

ttcccgacaa cgacattgat cagcagtacc aaggggcaaa cgggtcatat tctaggggct 960

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gcaggatatta tcgaattgat taattgttta gcggcaatag aggaacagac tgtaccagca 1020
actaaaaatg agattgggat agaaggtttt ccagaaaatt ttgtctatca tcaaaagaga 1080
gaatacccaa taagaatgc tttaaatttt tcgtttgctt ttggtggaaa taatagtgg 1140
gtcttattgt catctttaga ttcacctcta gaaacattac ctgctagaga aaatcttaaa 1200
atggctatct tatcatctgt tgcttcatt tetaagaatg aatcactttc tataacctat 1260
gaaaaagtgt ctagtaattt caacgacttt gaagcattac gctttaaagg ggctagacca 1320
cccaaaactg tcaaccagc acaatttagg aaaatggatg atttttccaa aatggttgcc 1380
gtaacaacag ctcaagcact aatagaaagc aatattaatc taaaaaaca agatacttca 1440
aaagtaggaa ttgtatttac aacactttct ggaccagttg aggttggtga aggtattgaa 1500
aagcaaatca caacagaagg atatgcacat gtttctgctt cagcattccc gtttacagta 1560
atgaatgcag cagctgggat gctttctatc atttttaaaa taacaggtcc ttatctgtc 1620
atttcgacaa atagtggagc gcttgatggg atacaatatg ccaaggaaat gatgcgtaac 1680
gataatctag actatgtgat tcttgtttct gctaatacgt ggacagacat gagttttatg 1740
tggtggcaac aattaaacta tgatagtcaa atgtttgtcg gttctgatta ttgttcagca 1800
caagtcctct ctgcgcaagc attggataat tctcctataa tattaggtag taaacaatta 1860
aaatatagcc ataaaacatt cacagatgtg atgactatct ttgatgctgc gcttcaaat 1920
ttattatcag acttaggact aaccataaaa gatatcaaag gtttcgtttg gaatgagcgg 1980
aagaaggcag ttagttcaga ttatgatttc ttagcgaact tgtctgagta ttataatatg 2040
ccaaaccttg cttctgggtc gtttggattt tcactaatg gtgctgggtga agaactggac 2100
tatactgtta atgaaagtat agaaaagggc tattatttag tcctatctta ttcgatcttc 2160
ggtggtatct cttttgctat tattgaaaaa agg 2193

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<210> SEQ ID NO 45

<211> LENGTH: 731

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 45

```

Met Ser Val Tyr Val Ser Gly Ile Gly Ile Ile Ser Ser Leu Gly Lys
 1             5             10             15
Asn Tyr Ser Glu His Lys Gln His Leu Phe Asp Leu Lys Glu Gly Ile
 20            25            30
Ser Lys His Leu Tyr Lys Asn His Asp Ser Ile Leu Glu Ser Tyr Thr
 35            40            45
Gly Ser Ile Thr Ser Asp Pro Glu Val Pro Glu Gln Tyr Lys Asp Glu
 50            55            60
Thr Arg Asn Phe Lys Phe Ala Phe Thr Ala Phe Glu Glu Ala Leu Ala
 65            70            75            80
Ser Ser Gly Val Asn Leu Lys Ala Tyr His Asn Ile Ala Val Cys Leu
 85            90            95
Gly Thr Ser Leu Gly Gly Lys Ser Ala Gly Gln Asn Ala Leu Tyr Gln
100           105           110
Phe Glu Glu Gly Glu Arg Gln Val Asp Ala Ser Leu Leu Glu Lys Ala
115           120           125
Ser Val Tyr His Ile Ala Asp Glu Leu Met Ala Tyr His Asp Ile Val
130           135           140
Gly Ala Ser Tyr Val Ile Ser Thr Ala Cys Ser Ala Ser Asn Asn Ala

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145	150	155	160
Val Ile Leu Gly Thr Gln Leu Leu Gln Asp Gly Asp Cys Asp Leu Ala			
	165	170	175
Ile Cys Gly Gly Cys Asp Glu Leu Ser Asp Ile Ser Leu Ala Gly Phe			
	180	185	190
Thr Ser Leu Gly Ala Ile Asn Thr Glu Met Ala Cys Gln Pro Tyr Ser			
	195	200	205
Ser Gly Lys Gly Ile Asn Leu Gly Glu Gly Ala Gly Phe Val Val Leu			
	210	215	220
Val Lys Asp Gln Ser Leu Ala Lys Tyr Gly Lys Ile Ile Gly Gly Leu			
	225	230	235
Ile Thr Ser Asp Gly Tyr His Ile Thr Ala Pro Lys Pro Thr Gly Glu			
	245	250	255
Gly Ala Ala Gln Ile Ala Lys Gln Leu Val Thr Gln Ala Gly Ile Asp			
	260	265	270
Tyr Ser Glu Ile Asp Tyr Ile Asn Gly His Gly Thr Gly Thr Gln Ala			
	275	280	285
Asn Asp Lys Met Glu Lys Asn Met Tyr Gly Lys Phe Phe Pro Thr Thr			
	290	295	300
Thr Leu Ile Ser Ser Thr Lys Gly Gln Thr Gly His Thr Leu Gly Ala			
	305	310	315
Ala Gly Ile Ile Glu Leu Ile Asn Cys Leu Ala Ala Ile Glu Glu Gln			
	325	330	335
Thr Val Pro Ala Thr Lys Asn Glu Ile Gly Ile Glu Gly Phe Pro Glu			
	340	345	350
Asn Phe Val Tyr His Gln Lys Arg Glu Tyr Pro Ile Arg Asn Ala Leu			
	355	360	365
Asn Phe Ser Phe Ala Phe Gly Gly Asn Asn Ser Gly Val Leu Leu Ser			
	370	375	380
Ser Leu Asp Ser Pro Leu Glu Thr Leu Pro Ala Arg Glu Asn Leu Lys			
	385	390	395
Met Ala Ile Leu Ser Ser Val Ala Ser Ile Ser Lys Asn Glu Ser Leu			
	405	410	415
Ser Ile Thr Tyr Glu Lys Val Ala Ser Asn Phe Asn Asp Phe Glu Ala			
	420	425	430
Leu Arg Phe Lys Gly Ala Arg Pro Pro Lys Thr Val Asn Pro Ala Gln			
	435	440	445
Phe Arg Lys Met Asp Asp Phe Ser Lys Met Val Ala Val Thr Thr Ala			
	450	455	460
Gln Ala Leu Ile Glu Ser Asn Ile Asn Leu Lys Lys Gln Asp Thr Ser			
	465	470	475
Lys Val Gly Ile Val Phe Thr Thr Leu Ser Gly Pro Val Glu Val Val			
	485	490	495
Glu Gly Ile Glu Lys Gln Ile Thr Thr Glu Gly Tyr Ala His Val Ser			
	500	505	510
Ala Ser Arg Phe Pro Phe Thr Val Met Asn Ala Ala Ala Gly Met Leu			
	515	520	525
Ser Ile Ile Phe Lys Ile Thr Gly Pro Leu Ser Val Ile Ser Thr Asn			
	530	535	540
Ser Gly Ala Leu Asp Gly Ile Gln Tyr Ala Lys Glu Met Met Arg Asn			
	545	550	555
Asp Asn Leu Asp Tyr Val Ile Leu Val Ser Ala Asn Gln Trp Thr Asp			
	565	570	575

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Met Ser Phe Met Trp Trp Gln Gln Leu Asn Tyr Asp Ser Gln Met Phe
      580                      585                      590

Val Gly Ser Asp Tyr Cys Ser Ala Gln Val Leu Ser Arg Gln Ala Leu
      595                      600                      605

Asp Asn Ser Pro Ile Ile Leu Gly Ser Lys Gln Leu Lys Tyr Ser His
      610                      615                      620

Lys Thr Phe Thr Asp Val Met Thr Ile Phe Asp Ala Ala Leu Gln Asn
      625                      630                      635                      640

Leu Leu Ser Asp Leu Gly Leu Thr Ile Lys Asp Ile Lys Gly Phe Val
      645                      650                      655

Trp Asn Glu Arg Lys Lys Ala Val Ser Ser Asp Tyr Asp Phe Leu Ala
      660                      665                      670

Asn Leu Ser Glu Tyr Tyr Asn Met Pro Asn Leu Ala Ser Gly Gln Phe
      675                      680                      685

Gly Phe Ser Ser Asn Gly Ala Gly Glu Glu Leu Asp Tyr Thr Val Asn
      690                      695                      700

Glu Ser Ile Glu Lys Gly Tyr Tyr Leu Val Leu Ser Tyr Ser Ile Phe
      705                      710                      715                      720

Gly Gly Ile Ser Phe Ala Ile Ile Glu Lys Arg
      725                      730

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<210> SEQ ID NO 46

<211> LENGTH: 727

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 46

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Val Ser Gly Ile Gly Ile Ile Ser Ser Leu Gly Lys Asn Tyr Ser Glu
  1                      5                      10                      15

His Lys Gln His Leu Phe Asp Leu Lys Glu Gly Ile Ser Lys His Leu
  20                      25                      30

Tyr Lys Asn His Asp Ser Ile Leu Glu Ser Tyr Thr Gly Ser Ile Thr
  35                      40                      45

Ser Asp Pro Glu Val Pro Glu Gln Tyr Lys Asp Glu Thr Arg Asn Phe
  50                      55                      60

Lys Phe Ala Phe Thr Ala Phe Glu Glu Ala Leu Ala Ser Ser Gly Val
  65                      70                      75                      80

Asn Leu Lys Ala Tyr His Asn Ile Ala Val Cys Leu Gly Thr Ser Leu
  85                      90                      95

Gly Gly Lys Ser Ala Gly Gln Asn Ala Leu Tyr Gln Phe Glu Glu Gly
  100                     105                     110

Glu Arg Gln Val Asp Ala Ser Leu Leu Glu Lys Ala Ser Val Tyr His
  115                     120                     125

Ile Ala Asp Glu Leu Met Ala Tyr His Asp Ile Val Gly Ala Ser Tyr
  130                     135                     140

Val Ile Ser Thr Ala Cys Ser Ala Ser Asn Asn Ala Val Ile Leu Gly
  145                     150                     155                     160

Thr Gln Leu Leu Gln Asp Gly Asp Cys Asp Leu Ala Ile Cys Gly Gly
  165                     170                     175

Cys Asp Glu Leu Ser Asp Ile Ser Leu Ala Gly Phe Thr Ser Leu Gly
  180                     185                     190

Ala Ile Asn Thr Glu Met Ala Cys Gln Pro Tyr Ser Ser Gly Lys Gly
  195                     200                     205

Ile Asn Leu Gly Glu Gly Ala Gly Phe Val Val Leu Val Lys Asp Gln

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210	215	220
Ser Leu Ala Lys Tyr Gly Lys Ile Ile Gly Gly Leu Ile Thr Ser Asp 225 230 235 240		
Gly Tyr His Ile Thr Ala Pro Lys Pro Thr Gly Glu Gly Ala Ala Gln 245 250 255		
Ile Ala Lys Gln Leu Val Thr Gln Ala Gly Ile Asp Tyr Ser Glu Ile 260 265 270		
Asp Tyr Ile Asn Gly His Gly Thr Gly Thr Gln Ala Asn Asp Lys Met 275 280 285		
Glu Lys Asn Met Tyr Gly Lys Phe Phe Pro Thr Thr Thr Leu Ile Ser 290 295 300		
Ser Thr Lys Gly Gln Thr Gly His Thr Leu Gly Ala Ala Gly Ile Ile 305 310 315 320		
Glu Leu Ile Asn Cys Leu Ala Ala Ile Glu Glu Gln Thr Val Pro Ala 325 330 335		
Thr Lys Asn Glu Ile Gly Ile Glu Gly Phe Pro Glu Asn Phe Val Tyr 340 345 350		
His Gln Lys Arg Glu Tyr Pro Ile Arg Asn Ala Leu Asn Phe Ser Phe 355 360 365		
Ala Phe Gly Gly Asn Asn Ser Gly Val Leu Leu Ser Ser Leu Asp Ser 370 375 380		
Pro Leu Glu Thr Leu Pro Ala Arg Glu Asn Leu Lys Met Ala Ile Leu 385 390 395 400		
Ser Ser Val Ala Ser Ile Ser Lys Asn Glu Ser Leu Ser Ile Thr Tyr 405 410 415		
Glu Lys Val Ala Ser Asn Phe Asn Asp Phe Glu Ala Leu Arg Phe Lys 420 425 430		
Gly Ala Arg Pro Pro Lys Thr Val Asn Pro Ala Gln Phe Arg Lys Met 435 440 445		
Asp Asp Phe Ser Lys Met Val Ala Val Thr Thr Ala Gln Ala Leu Ile 450 455 460		
Glu Ser Asn Ile Asn Leu Lys Lys Gln Asp Thr Ser Lys Val Gly Ile 465 470 475 480		
Val Phe Thr Thr Leu Ser Gly Pro Val Glu Val Val Glu Gly Ile Glu 485 490 495		
Lys Gln Ile Thr Thr Glu Gly Tyr Ala His Val Ser Ala Ser Arg Phe 500 505 510		
Pro Phe Thr Val Met Asn Ala Ala Ala Gly Met Leu Ser Ile Ile Phe 515 520 525		
Lys Ile Thr Gly Pro Leu Ser Val Ile Ser Thr Asn Ser Gly Ala Leu 530 535 540		
Asp Gly Ile Gln Tyr Ala Lys Glu Met Met Arg Asn Asp Asn Leu Asp 545 550 555 560		
Tyr Val Ile Leu Val Ser Ala Asn Gln Trp Thr Asp Met Ser Phe Met 565 570 575		
Trp Trp Gln Gln Leu Asn Tyr Asp Ser Gln Met Phe Val Gly Ser Asp 580 585 590		
Tyr Cys Ser Ala Gln Val Leu Ser Arg Gln Ala Leu Asp Asn Ser Pro 595 600 605		
Ile Ile Leu Gly Ser Lys Gln Leu Lys Tyr Ser His Lys Thr Phe Thr 610 615 620		
Asp Val Met Thr Ile Phe Asp Ala Ala Leu Gln Asn Leu Leu Ser Asp 625 630 635 640		

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Leu Gly Leu Thr Ile Lys Asp Ile Lys Gly Phe Val Trp Asn Glu Arg
645 650 655

Lys Lys Ala Val Ser Ser Asp Tyr Asp Phe Leu Ala Asn Leu Ser Glu
660 665 670

Tyr Tyr Asn Met Pro Asn Leu Ala Ser Gly Gln Phe Gly Phe Ser Ser
675 680 685

Asn Gly Ala Gly Glu Glu Leu Asp Tyr Thr Val Asn Glu Ser Ile Glu
690 695 700

Lys Gly Tyr Tyr Leu Val Leu Ser Tyr Ser Ile Phe Gly Gly Ile Ser
705 710 715 720

Phe Ala Ile Ile Glu Lys Arg
725

<210> SEQ ID NO 47
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 47

atgaaaatag atgacctaa gaaaagcgac aatgttgaag atcgctcgctc cagtagcgga 60
ggttcattct ctacggagg aagtggatta cggattcttc aacttttatt gctgagagg 120
agttgaaaa ccaagcttgt ggttttaatc atcttactgc tacttgccgg agggggacta 180
accagcattt ttaatgactc atcctcacct tctagttacc aatctcagaa tgtctcacgt 240
tctgttgata atagcgcaac gagagaacaa atcgatttcg ttaataaagt ccttggtctca 300
actgaggatt tctggtcaca agaattccaa acccaaggtt ttggaaatta taaggaacca 360
aaacttggtc ttacaccaa ttcaattcaa acagggttggt gtataggtga atctgcttca 420
ggaccatttt attgttcagc agataaaaa atctatcttg atatttcttt ttacaatgaa 480
ttatcacata aatatggtgc tactggtgat ttgctatgg cctacgtcat cggcccgaa 540
gttggtcacc acattcaaac agagttaggc attatggata agtataatag aatgagacac 600
ggacttacta agaaagaagc aaatgcttta aatgttcggc tagaacttca agcagattat 660
tatgcagggg tatgggtcct ctacatcagg ggaaaaaatc tcttagaaca aggagacttt 720
gaagaggcca tgaatgctgc ccacgccgc ggagacgata cccttcagaa agaaacctac 780
ggaaaattag tgccgatag ctttaccat ggaacagctg aacaacgcca acgttggttt 840
aacaaggct ttcaatatgg tgacatcaa caggtgata cttctccgt agaactcta 900

<210> SEQ ID NO 48
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 48

Met Lys Ile Asp Asp Leu Arg Lys Ser Asp Asn Val Glu Asp Arg Arg
1 5 10 15

Ser Ser Ser Gly Gly Ser Phe Ser Ser Gly Gly Ser Gly Leu Pro Ile
20 25 30

Leu Gln Leu Leu Leu Leu Arg Gly Ser Trp Lys Thr Lys Leu Val Val
35 40 45

Leu Ile Ile Leu Leu Leu Leu Gly Gly Gly Gly Leu Thr Ser Ile Phe
50 55 60

Asn Asp Ser Ser Ser Pro Ser Ser Tyr Gln Ser Gln Asn Val Ser Arg
65 70 75 80

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tatccagaag cagaagcaaa caacaatgac tctaataacg gctctagtgc tgtaaattat	900
aaatataaag tagatattac tagccctctc gatgcattaa aacaagggtt taccgatatca	960
gttgaagtag ttaatggaga taagcacctt attgtcccta caagttctgt gataaacaaa	1020
gataataaac actttgtttg ggtatacaat gattctaata gtaaaatttc caaagttgaa	1080
gtcaaaattg gtaaagctga tgctaagaca caagaaattt tatcagggtt gaaagcagga	1140
caaatcgtgg ttactaatcc aagtaaaacc ttcaaggatg ggcaaaaaat tgataatatt	1200
gaatcaatcg atcttaactc taataagaaa tcagaggtga aa	1242

<210> SEQ ID NO 50

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 50

Met	Ser	Lys	Arg	Gln	Asn	Leu	Gly	Ile	Ser	Lys	Lys	Gly	Ala	Ile	Ile
1				5					10					15	
Ser	Gly	Leu	Ser	Val	Ala	Leu	Ile	Val	Val	Ile	Gly	Gly	Phe	Leu	Trp
			20					25					30		
Val	Gln	Ser	Gln	Pro	Asn	Lys	Ser	Ala	Val	Lys	Thr	Asn	Tyr	Lys	Val
		35					40					45			
Phe	Asn	Val	Arg	Glu	Gly	Ser	Val	Ser	Ser	Ser	Thr	Leu	Leu	Thr	Gly
	50					55					60				
Lys	Ala	Lys	Ala	Asn	Gln	Glu	Gln	Tyr	Val	Tyr	Phe	Asp	Ala	Asn	Lys
65					70					75				80	
Gly	Asn	Arg	Ala	Thr	Val	Thr	Val	Lys	Val	Gly	Asp	Lys	Ile	Thr	Ala
			85					90						95	
Gly	Gln	Gln	Leu	Val	Gln	Tyr	Asp	Thr	Thr	Thr	Ala	Gln	Ala	Ala	Tyr
			100					105					110		
Asp	Thr	Ala	Asn	Arg	Gln	Leu	Asn	Lys	Val	Ala	Arg	Gln	Ile	Asn	Asn
		115					120					125			
Leu	Lys	Thr	Thr	Gly	Ser	Leu	Pro	Ala	Met	Glu	Ser	Ser	Asp	Gln	Ser
		130				135					140				
Ser	Ser	Ser	Ser	Gln	Gly	Gln	Gly	Thr	Gln	Ser	Thr	Ser	Gly	Ala	Thr
145					150					155				160	
Asn	Arg	Leu	Gln	Gln	Asn	Tyr	Gln	Ser	Gln	Ala	Asn	Ala	Ser	Tyr	Asn
			165					170						175	
Gln	Gln	Leu	Gln	Asp	Leu	Asn	Asp	Ala	Tyr	Ala	Asp	Ala	Gln	Ala	Glu
		180						185					190		
Val	Asn	Lys	Ala	Gln	Lys	Ala	Leu	Asn	Asp	Thr	Val	Ile	Thr	Ser	Asp
		195					200					205			
Val	Ser	Gly	Thr	Val	Val	Glu	Val	Asn	Ser	Asp	Ile	Asp	Pro	Ala	Ser
		210				215					220				
Lys	Thr	Ser	Gln	Val	Leu	Val	His	Val	Ala	Thr	Glu	Gly	Lys	Leu	Gln
225				230					235					240	
Val	Gln	Gly	Thr	Met	Ser	Glu	Tyr	Asp	Leu	Ala	Asn	Val	Lys	Lys	Asp
			245						250					255	
Gln	Ala	Val	Lys	Ile	Lys	Ser	Lys	Val	Tyr	Pro	Asp	Lys	Glu	Trp	Glu
		260						265					270		
Gly	Lys	Ile	Ser	Tyr	Ile	Ser	Asn	Tyr	Pro	Glu	Ala	Glu	Ala	Asn	Asn
		275					280					285			
Asn	Asp	Ser	Asn	Asn	Gly	Ser	Ser	Ala	Val	Asn	Tyr	Lys	Tyr	Lys	Val
		290				295					300				

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Asp Ile Thr Ser Pro Leu Asp Ala Leu Lys Gln Gly Phe Thr Val Ser
305          310          315          320

Val Glu Val Val Asn Gly Asp Lys His Leu Ile Val Pro Thr Ser Ser
          325          330          335

Val Ile Asn Lys Asp Asn Lys His Phe Val Trp Val Tyr Asn Asp Ser
          340          345          350

Asn Arg Lys Ile Ser Lys Val Glu Val Lys Ile Gly Lys Ala Asp Ala
          355          360          365

Lys Thr Gln Glu Ile Leu Ser Gly Leu Lys Ala Gly Gln Ile Val Val
          370          375          380

Thr Asn Pro Ser Lys Thr Phe Lys Asp Gly Gln Lys Ile Asp Asn Ile
385          390          395          400

Glu Ser Ile Asp Leu Asn Ser Asn Lys Lys Ser Glu Val Lys
          405          410

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<210> SEQ ID NO 51
<211> LENGTH: 385
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 51

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Phe Leu Trp Val Gln Ser Gln Pro Asn Lys Ser Ala Val Lys Thr Asn
 1          5          10          15

Tyr Lys Val Phe Asn Val Arg Glu Gly Ser Val Ser Ser Ser Thr Leu
 20          25          30

Leu Thr Gly Lys Ala Lys Ala Asn Gln Glu Gln Tyr Val Tyr Phe Asp
 35          40          45

Ala Asn Lys Gly Asn Arg Ala Thr Val Thr Val Lys Val Gly Asp Lys
 50          55          60

Ile Thr Ala Gly Gln Gln Leu Val Gln Tyr Asp Thr Thr Thr Ala Gln
 65          70          75          80

Ala Ala Tyr Asp Thr Ala Asn Arg Gln Leu Asn Lys Val Ala Arg Gln
 85          90          95

Ile Asn Asn Leu Lys Thr Thr Gly Ser Leu Pro Ala Met Glu Ser Ser
100          105          110

Asp Gln Ser Ser Ser Ser Ser Gln Gly Gln Gly Thr Gln Ser Thr Ser
115          120          125

Gly Ala Thr Asn Arg Leu Gln Gln Asn Tyr Gln Ser Gln Ala Asn Ala
130          135          140

Ser Tyr Asn Gln Gln Leu Gln Asp Leu Asn Asp Ala Tyr Ala Asp Ala
145          150          155          160

Gln Ala Glu Val Asn Lys Ala Gln Lys Ala Leu Asn Asp Thr Val Ile
165          170          175

Thr Ser Asp Val Ser Gly Thr Val Val Glu Val Asn Ser Asp Ile Asp
180          185          190

Pro Ala Ser Lys Thr Ser Gln Val Leu Val His Val Ala Thr Glu Gly
195          200          205

Lys Leu Gln Val Gln Gly Thr Met Ser Glu Tyr Asp Leu Ala Asn Val
210          215          220

Lys Lys Asp Gln Ala Val Lys Ile Lys Ser Lys Val Tyr Pro Asp Lys
225          230          235          240

Glu Trp Glu Gly Lys Ile Ser Tyr Ile Ser Asn Tyr Pro Glu Ala Glu
245          250          255

Ala Asn Asn Asn Asp Ser Asn Asn Gly Ser Ser Ala Val Asn Tyr Lys
260          265          270

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Tyr Lys Val Asp Ile Thr Ser Pro Leu Asp Ala Leu Lys Gln Gly Phe
 275 280 285
 Thr Val Ser Val Glu Val Val Asn Gly Asp Lys His Leu Ile Val Pro
 290 295 300
 Thr Ser Ser Val Ile Asn Lys Asp Asn Lys His Phe Val Trp Val Tyr
 305 310 315 320
 Asn Asp Ser Asn Arg Lys Ile Ser Lys Val Glu Val Lys Ile Gly Lys
 325 330 335
 Ala Asp Ala Lys Thr Gln Glu Ile Leu Ser Gly Leu Lys Ala Gly Gln
 340 345 350
 Ile Val Val Thr Asn Pro Ser Lys Thr Phe Lys Asp Gly Gln Lys Ile
 355 360 365
 Asp Asn Ile Glu Ser Ile Asp Leu Asn Ser Asn Lys Lys Ser Glu Val
 370 375 380
 Lys
 385

<210> SEQ ID NO 52
 <211> LENGTH: 930
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 52

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atgaaaaaa ttggaattat tgtcctcaca ctactgacct tctttttggt atcttgcgga    60
caacaaacta aacaagaaag cactaaaaca actatttcta aaatgcctaa aattgaaggc    120
ttcacctatt atggaaaaat tcctgaaaaat ccgaaaaaag taattaattt tacatatctt    180
tactactgggt atttattaaa actaggtggt aatgtttcaa gttacagttt agacttagaa    240
aaagatagcc cggtttttgg taaacaactg aaagaagcta aaaaattaac tgctgatgat    300
acagaagcta ttgccgcaca aaaacctgat ttaatcatgg ttttcgatca agatccaaac    360
atcaatactc tgaaaaaaat tgcaccaact ttagttatta aatatggtgc acaaaattat    420
ttagatatga tgccagcctt ggggaaaagta ttcggtaaag aaaagaagc taatcagtggt    480
gttagccaat ggaaaactaa aactctcgct gtcaaaaaag atttacacca tatcttaaag    540
cctaacacta cttttactat tatggatttt tatgataaaa atatctattt atatggtaat    600
aattttggac gcggtggaga actaatctat gattcactag gttatgctgc cccagaaaaa    660
gtcaaaaaag atgtctttaa aaaagggtgg tttaccgttt cgcaagaagc aatcggtgat    720
tacgttgagg attatgccct tgtaatatata aacaaaacga ctaaaaaagc agcttcatca    780
cttaaagaaa gtgatgtctg gaagaattta ccagctgtca aaaaagggca catcatagaa    840
agtaactacg acgtgtttta tttctctgac cctctatett tagaagctca attaaaatca    900
tttacaaggg ctatcaaaga aaatacaaat                                930
  
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<210> SEQ ID NO 53
 <211> LENGTH: 310
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 53

Met Lys Lys Ile Gly Ile Ile Val Leu Thr Leu Leu Thr Phe Phe Leu
 1 5 10 15
 Val Ser Cys Gly Gln Gln Thr Lys Gln Glu Ser Thr Lys Thr Thr Ile
 20 25 30

-continued

Ser Lys Met Pro Lys Ile Glu Gly Phe Thr Tyr Tyr Gly Lys Ile Pro
 35 40 45
 Glu Asn Pro Lys Lys Val Ile Asn Phe Thr Tyr Ser Tyr Thr Gly Tyr
 50 55 60
 Leu Leu Lys Leu Gly Val Asn Val Ser Ser Tyr Ser Leu Asp Leu Glu
 65 70 75 80
 Lys Asp Ser Pro Val Phe Gly Lys Gln Leu Lys Glu Ala Lys Lys Leu
 85 90 95
 Thr Ala Asp Asp Thr Glu Ala Ile Ala Ala Gln Lys Pro Asp Leu Ile
 100 105 110
 Met Val Phe Asp Gln Asp Pro Asn Ile Asn Thr Leu Lys Lys Ile Ala
 115 120 125
 Pro Thr Leu Val Ile Lys Tyr Gly Ala Gln Asn Tyr Leu Asp Met Met
 130 135 140
 Pro Ala Leu Gly Lys Val Phe Gly Lys Glu Lys Glu Ala Asn Gln Trp
 145 150 155 160
 Val Ser Gln Trp Lys Thr Lys Thr Leu Ala Val Lys Lys Asp Leu His
 165 170 175
 His Ile Leu Lys Pro Asn Thr Thr Phe Thr Ile Met Asp Phe Tyr Asp
 180 185 190
 Lys Asn Ile Tyr Leu Tyr Gly Asn Asn Phe Gly Arg Gly Gly Glu Leu
 195 200 205
 Ile Tyr Asp Ser Leu Gly Tyr Ala Ala Pro Glu Lys Val Lys Lys Asp
 210 215 220
 Val Phe Lys Lys Gly Trp Phe Thr Val Ser Gln Glu Ala Ile Gly Asp
 225 230 235 240
 Tyr Val Gly Asp Tyr Ala Leu Val Asn Ile Asn Lys Thr Thr Lys Lys
 245 250 255
 Ala Ala Ser Ser Leu Lys Glu Ser Asp Val Trp Lys Asn Leu Pro Ala
 260 265 270
 Val Lys Lys Gly His Ile Ile Glu Ser Asn Tyr Asp Val Phe Tyr Phe
 275 280 285
 Ser Asp Pro Leu Ser Leu Glu Ala Gln Leu Lys Ser Phe Thr Lys Ala
 290 295 300
 Ile Lys Glu Asn Thr Asn
 305 310

<210> SEQ ID NO 54

<211> LENGTH: 272

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 54

Glu Gly Phe Thr Tyr Tyr Gly Lys Ile Pro Glu Asn Pro Lys Lys Val
 1 5 10 15
 Ile Asn Phe Thr Tyr Ser Tyr Thr Gly Tyr Leu Leu Lys Leu Gly Val
 20 25 30
 Asn Val Ser Ser Tyr Ser Leu Asp Leu Glu Lys Asp Ser Pro Val Phe
 35 40 45
 Gly Lys Gln Leu Lys Glu Ala Lys Lys Leu Thr Ala Asp Asp Thr Glu
 50 55 60
 Ala Ile Ala Ala Gln Lys Pro Asp Leu Ile Met Val Phe Asp Gln Asp
 65 70 75 80
 Pro Asn Ile Asn Thr Leu Lys Lys Ile Ala Pro Thr Leu Val Ile Lys
 85 90 95

-continued

Tyr Gly Ala Gln Asn Tyr Leu Asp Met Met Pro Ala Leu Gly Lys Val
 100 105 110
 Phe Gly Lys Glu Lys Glu Ala Asn Gln Trp Val Ser Gln Trp Lys Thr
 115 120 125
 Lys Thr Leu Ala Val Lys Lys Asp Leu His His Ile Leu Lys Pro Asn
 130 135 140
 Thr Thr Phe Thr Ile Met Asp Phe Tyr Asp Lys Asn Ile Tyr Leu Tyr
 145 150 155 160
 Gly Asn Asn Phe Gly Arg Gly Gly Glu Leu Ile Tyr Asp Ser Leu Gly
 165 170 175
 Tyr Ala Ala Pro Glu Lys Val Lys Lys Asp Val Phe Lys Lys Gly Trp
 180 185 190
 Phe Thr Val Ser Gln Glu Ala Ile Gly Asp Tyr Val Gly Asp Tyr Ala
 195 200 205
 Leu Val Asn Ile Asn Lys Thr Thr Lys Lys Ala Ala Ser Ser Leu Lys
 210 215 220
 Glu Ser Asp Val Trp Lys Asn Leu Pro Ala Val Lys Lys Gly His Ile
 225 230 235 240
 Ile Glu Ser Asn Tyr Asp Val Phe Tyr Phe Ser Asp Pro Leu Ser Leu
 245 250 255
 Glu Ala Gln Leu Lys Ser Phe Thr Lys Ala Ile Lys Glu Asn Thr Asn
 260 265 270

<210> SEQ ID NO 55

<211> LENGTH: 302

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 55

Met Lys Lys Ile Gly Ile Ile Val Leu Thr Leu Leu Thr Phe Phe Leu
 1 5 10 15
 Val Ser Cys Gly Gln Gln Thr Lys Gln Glu Ser Thr Lys Thr Thr Ile
 20 25 30
 Ser Lys Met Pro Lys Ile Glu Gly Phe Thr Tyr Tyr Gly Lys Ile Pro
 35 40 45
 Glu Asn Pro Lys Lys Val Ile Asn Phe Thr Tyr Ser Tyr Thr Gly Tyr
 50 55 60
 Leu Leu Lys Leu Gly Val Asn Val Ser Ser Tyr Ser Leu Asp Leu Glu
 65 70 75 80
 Lys Asp Ser Pro Val Phe Gly Lys Gln Leu Lys Glu Ala Lys Lys Leu
 85 90 95
 Thr Ala Asp Asp Thr Glu Ala Ile Ala Ala Gln Lys Pro Asp Leu Ile
 100 105 110
 Met Val Phe Asp Gln Asp Pro Asn Ile Asn Thr Leu Lys Lys Ile Ala
 115 120 125
 Pro Thr Leu Val Ile Lys Tyr Gly Ala Gln Asn Tyr Leu Asp Met Met
 130 135 140
 Pro Ala Leu Gly Lys Val Phe Gly Lys Glu Lys Glu Ala Asn Gln Trp
 145 150 155 160
 Val Ser Gln Trp Lys Thr Lys Thr Leu Ala Val Lys Lys Asp Leu His
 165 170 175
 His Ile Leu Lys Pro Asn Thr Thr Phe Thr Ile Met Asp Phe Tyr Asp
 180 185 190
 Lys Asn Ile Tyr Leu Tyr Gly Asn Asn Phe Gly Arg Gly Gly Glu Leu

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195					200					205					
Ile	Tyr	Asp	Ser	Leu	Gly	Tyr	Ala	Ala	Pro	Glu	Lys	Val	Lys	Lys	Asp
210					215					220					
Val	Phe	Lys	Lys	Gly	Trp	Phe	Thr	Val	Ser	Gln	Glu	Ala	Ile	Gly	Asp
225					230					235					240
Tyr	Val	Gly	Asp	Tyr	Ala	Leu	Val	Asn	Ile	Asn	Lys	Thr	Thr	Lys	Lys
				245					250					255	
Ala	Ala	Ser	Ser	Leu	Lys	Glu	Ser	Asp	Val	Trp	Lys	Asn	Leu	Pro	Ala
				260					265					270	
Val	Lys	Lys	Gly	His	Ile	Ile	Glu	Ser	Asn	Tyr	Asp	Val	Phe	Tyr	Phe
				275					280					285	
Ser	Asp	Pro	Leu	Ser	Leu	Glu	Ala	Gln	Leu	Lys	Ser	Phe	Thr		
				290					295					300	
<210> SEQ ID NO 56															
<211> LENGTH: 264															
<212> TYPE: PRT															
<213> ORGANISM: Streptococcus agalactiae															
<400> SEQUENCE: 56															
Glu	Gly	Phe	Thr	Tyr	Tyr	Gly	Lys	Ile	Pro	Glu	Asn	Pro	Lys	Lys	Val
1				5					10					15	
Ile	Asn	Phe	Thr	Tyr	Ser	Tyr	Thr	Gly	Tyr	Leu	Leu	Lys	Leu	Gly	Val
				20					25					30	
Asn	Val	Ser	Ser	Tyr	Ser	Leu	Asp	Leu	Glu	Lys	Asp	Ser	Pro	Val	Phe
				35					40					45	
Gly	Lys	Gln	Leu	Lys	Glu	Ala	Lys	Lys	Leu	Thr	Ala	Asp	Asp	Thr	Glu
				50					55					60	
Ala	Ile	Ala	Ala	Gln	Lys	Pro	Asp	Leu	Ile	Met	Val	Phe	Asp	Gln	Asp
				65					70					75	80
Pro	Asn	Ile	Asn	Thr	Leu	Lys	Lys	Ile	Ala	Pro	Thr	Leu	Val	Ile	Lys
				85					90					95	
Tyr	Gly	Ala	Gln	Asn	Tyr	Leu	Asp	Met	Met	Pro	Ala	Leu	Gly	Lys	Val
				100					105					110	
Phe	Gly	Lys	Glu	Lys	Glu	Ala	Asn	Gln	Trp	Val	Ser	Gln	Trp	Lys	Thr
				115					120					125	
Lys	Thr	Leu	Ala	Val	Lys	Lys	Asp	Leu	His	His	Ile	Leu	Lys	Pro	Asn
				130					135					140	
Thr	Thr	Phe	Thr	Ile	Met	Asp	Phe	Tyr	Asp	Lys	Asn	Ile	Tyr	Leu	Tyr
				145					150					155	160
Gly	Asn	Asn	Phe	Gly	Arg	Gly	Gly	Glu	Leu	Ile	Tyr	Asp	Ser	Leu	Gly
				165					170					175	
Tyr	Ala	Ala	Pro	Glu	Lys	Val	Lys	Lys	Asp	Val	Phe	Lys	Lys	Gly	Trp
				180					185					190	
Phe	Thr	Val	Ser	Gln	Glu	Ala	Ile	Gly	Asp	Tyr	Val	Gly	Asp	Tyr	Ala
				195					200					205	
Leu	Val	Asn	Ile	Asn	Lys	Thr	Thr	Lys	Lys	Ala	Ala	Ser	Ser	Leu	Lys
				210					215					220	
Glu	Ser	Asp	Val	Trp	Lys	Asn	Leu	Pro	Ala	Val	Lys	Lys	Gly	His	Ile
				225					230					235	240
Ile	Glu	Ser	Asn	Tyr	Asp	Val	Phe	Tyr	Phe	Ser	Asp	Pro	Leu	Ser	Leu
				245					250					255	
Glu	Ala	Gln	Leu	Lys	Ser	Phe	Thr								
				260											

-continued

<210> SEQ ID NO 57
<211> LENGTH: 576
<212> TYPE: DNA
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 57

atgaaagtga aaaataagat tttaacgatg gtagcactta ctgtcttaac atgtgctact 60
tattcatcaa tcggttatgc tgatacaagt gataagaata ctgacacgag tgcgtgact 120
acgaccttat ctgaggagaa aagatcagat gaactagacc agtctagtag tggttcttct 180
tctgaaaatg aatcgagttc atcaagtga ccagaaacaa atccgtcaac taatccacct 240
acaacagaac catcgcaacc ctcacctagt gaagagaaca agcctgatgg tagaacgaag 300
acagaaattg gcaataataa ggatatttct agtggaaaca aagtattaat ttcagaagat 360
agtattaaga attttagtaa agcaagtagt gatcaagaag aagtggatcg cgatgaatca 420
tcattcttcaa aagcaaatga tgggaaaaaa ggccacagta agcctaaaaa ggaacttcct 480
aaaacaggag atagccactc agatactgta atagcatcta cgggagggat tattctgtta 540
tcattaagtt ttacaataa gaaaatgaaa ctttat 576

<210> SEQ ID NO 58
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 58

Met Lys Val Lys Asn Lys Ile Leu Thr Met Val Ala Leu Thr Val Leu
1 5 10 15
Thr Cys Ala Thr Tyr Ser Ser Ile Gly Tyr Ala Asp Thr Ser Asp Lys
20 25 30
Asn Thr Asp Thr Ser Val Val Thr Thr Thr Leu Ser Glu Glu Lys Arg
35 40 45
Ser Asp Glu Leu Asp Gln Ser Ser Thr Gly Ser Ser Ser Glu Asn Glu
50 55 60
Ser Ser Ser Ser Ser Glu Pro Glu Thr Asn Pro Ser Thr Asn Pro Pro
65 70 75 80
Thr Thr Glu Pro Ser Gln Pro Ser Pro Ser Glu Glu Asn Lys Pro Asp
85 90 95
Gly Arg Thr Lys Thr Glu Ile Gly Asn Asn Lys Asp Ile Ser Ser Gly
100 105 110
Thr Lys Val Leu Ile Ser Glu Asp Ser Ile Lys Asn Phe Ser Lys Ala
115 120 125
Ser Ser Asp Gln Glu Glu Val Asp Arg Asp Glu Ser Ser Ser Ser Lys
130 135 140
Ala Asn Asp Gly Lys Lys Gly His Ser Lys Pro Lys Lys Glu Leu Pro
145 150 155 160
Lys Thr Gly Asp Ser His Ser Asp Thr Val Ile Ala Ser Thr Gly Gly
165 170 175
Ile Ile Leu Leu Ser Leu Ser Phe Tyr Asn Lys Lys Met Lys Leu Tyr
180 185 190

<210> SEQ ID NO 59
<211> LENGTH: 165
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 59

-continued

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Asp Thr Ser Asp Lys Asn Thr Asp Thr Ser Val Val Thr Thr Thr Leu
 1          5          10          15
Ser Glu Glu Lys Arg Ser Asp Glu Leu Asp Gln Ser Ser Thr Gly Ser
      20          25          30
Ser Ser Glu Asn Glu Ser Ser Ser Ser Ser Glu Pro Glu Thr Asn Pro
      35          40          45
Ser Thr Asn Pro Pro Thr Thr Glu Pro Ser Gln Pro Ser Pro Ser Glu
      50          55          60
Glu Asn Lys Pro Asp Gly Arg Thr Lys Thr Glu Ile Gly Asn Asn Lys
65          70          75          80
Asp Ile Ser Ser Gly Thr Lys Val Leu Ile Ser Glu Asp Ser Ile Lys
      85          90          95
Asn Phe Ser Lys Ala Ser Ser Asp Gln Glu Glu Val Asp Arg Asp Glu
      100          105          110
Ser Ser Ser Ser Lys Ala Asn Asp Gly Lys Lys Gly His Ser Lys Pro
      115          120          125
Lys Lys Glu Leu Pro Lys Thr Gly Asp Ser His Ser Asp Thr Val Ile
      130          135          140
Ala Ser Thr Gly Gly Ile Ile Leu Leu Ser Leu Ser Phe Tyr Asn Lys
145          150          155          160
Lys Met Lys Leu Tyr
      165

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<210> SEQ ID NO 60
<211> LENGTH: 140
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 60

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Asp Gln Ser Ser Thr Gly Ser Ser Ser Glu Asn Glu Ser Ser Ser Ser
 1          5          10          15
Ser Glu Pro Glu Thr Asn Pro Ser Thr Asn Pro Pro Thr Thr Glu Pro
      20          25          30
Ser Gln Pro Ser Pro Ser Glu Glu Asn Lys Pro Asp Gly Arg Thr Lys
      35          40          45
Thr Glu Ile Gly Asn Asn Lys Asp Ile Ser Ser Gly Thr Lys Val Leu
      50          55          60
Ile Ser Glu Asp Ser Ile Lys Asn Phe Ser Lys Ala Ser Ser Asp Gln
65          70          75          80
Glu Glu Val Asp Arg Asp Glu Ser Ser Ser Ser Lys Ala Asn Asp Gly
      85          90          95
Lys Lys Gly His Ser Lys Pro Lys Lys Glu Leu Pro Lys Thr Gly Asp
      100          105          110
Ser His Ser Asp Thr Val Ile Ala Ser Thr Gly Gly Ile Ile Leu Leu
      115          120          125
Ser Leu Ser Phe Tyr Asn Lys Lys Met Lys Leu Tyr
      130          135          140

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<210> SEQ ID NO 61
<211> LENGTH: 158
<212> TYPE: PRT
<213> ORGANISM: Streptococcus agalactiae

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<400> SEQUENCE: 61

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Met Lys Val Lys Asn Lys Ile Leu Thr Met Val Ala Leu Thr Val Leu
 1          5          10          15

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-continued

Thr Cys Ala Thr Tyr Ser Ser Ile Gly Tyr Ala Asp Thr Ser Asp Lys
 20 25 30
 Asn Thr Asp Thr Ser Val Val Thr Thr Thr Leu Ser Glu Glu Lys Arg
 35 40 45
 Ser Asp Glu Leu Asp Gln Ser Ser Thr Gly Ser Ser Ser Glu Asn Glu
 50 55 60
 Ser Ser Ser Ser Ser Glu Pro Glu Thr Asn Pro Ser Thr Asn Pro Pro
 65 70 75 80
 Thr Thr Glu Pro Ser Gln Pro Ser Pro Ser Glu Glu Asn Lys Pro Asp
 85 90 95
 Gly Arg Thr Lys Thr Glu Ile Gly Asn Asn Lys Asp Ile Ser Ser Gly
 100 105 110
 Thr Lys Val Leu Ile Ser Glu Asp Ser Ile Lys Asn Phe Ser Lys Ala
 115 120 125
 Ser Ser Asp Gln Glu Glu Val Asp Arg Asp Glu Ser Ser Ser Ser Lys
 130 135 140
 Ala Asn Asp Gly Lys Lys Gly His Ser Lys Pro Lys Lys Glu
 145 150 155

<210> SEQ ID NO 62
 <211> LENGTH: 131
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 62

Asp Thr Ser Asp Lys Asn Thr Asp Thr Ser Val Val Thr Thr Thr Leu
 1 5 10 15
 Ser Glu Glu Lys Arg Ser Asp Glu Leu Asp Gln Ser Ser Thr Gly Ser
 20 25 30
 Ser Ser Glu Asn Glu Ser Ser Ser Ser Ser Glu Pro Glu Thr Asn Pro
 35 40 45
 Ser Thr Asn Pro Pro Thr Thr Glu Pro Ser Gln Pro Ser Pro Ser Glu
 50 55 60
 Glu Asn Lys Pro Asp Gly Arg Thr Lys Thr Glu Ile Gly Asn Asn Lys
 65 70 75 80
 Asp Ile Ser Ser Gly Thr Lys Val Leu Ile Ser Glu Asp Ser Ile Lys
 85 90 95
 Asn Phe Ser Lys Ala Ser Ser Asp Gln Glu Glu Val Asp Arg Asp Glu
 100 105 110
 Ser Ser Ser Ser Lys Ala Asn Asp Gly Lys Lys Gly His Ser Lys Pro
 115 120 125
 Lys Lys Glu
 130

<210> SEQ ID NO 63
 <211> LENGTH: 106
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 63

Asp Gln Ser Ser Thr Gly Ser Ser Ser Glu Asn Glu Ser Ser Ser Ser
 1 5 10 15
 Ser Glu Pro Glu Thr Asn Pro Ser Thr Asn Pro Pro Thr Thr Glu Pro
 20 25 30
 Ser Gln Pro Ser Pro Ser Glu Glu Asn Lys Pro Asp Gly Arg Thr Lys
 35 40 45

-continued

Thr Glu Ile Gly Asn Asn Lys Asp Ile Ser Ser Gly Thr Lys Val Leu
 50 55 60
 Ile Ser Glu Asp Ser Ile Lys Asn Phe Ser Lys Ala Ser Ser Asp Gln
 65 70 75 80
 Glu Glu Val Asp Arg Asp Glu Ser Ser Ser Ser Lys Ala Asn Asp Gly
 85 90 95
 Lys Lys Gly His Ser Lys Pro Lys Lys Glu
 100 105

<210> SEQ ID NO 64
 <211> LENGTH: 924
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 64

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atgaaaagga tacggaaaag ccttatTTTT gttctcggag tagttaccct aatttgctta    60
tgtgcttgta ctaaacaagg ccagcaaaaa aatggcttgt cagtagtgac tagcttttat    120
ccagtatatt ccattacaaa agcagtttct ggtgatttga atgatattaa aatgattcga    180
tcacagtcag gtattcatgg ttttgaaccc tcatcaagtg atgttgctgc catttatgat    240
gctgatctat ttctttatca ttcgcacaca ctagaagctt gggcgagacg tttggaacct    300
agtttgcac actctaaagt atctgtaatt gaagcttcaa aaggtatgac tttggataaa    360
gttcatggct tagaagatgt agaggcagaa aaaggagtag atgagtcaac cttgtatgac    420
cctcacactt ggaatgaccc tgtaaaagta tctgaggaag cacaactcat cgctacacaa    480
ttagctaaaa aggatcctaa aaacgctaag gtttatcaaa aaaatgctga tcaatttagt    540
gacaaggcaa tggctattgc agagaagtat aagccaaaat ttaaagctgc aaagtctaaa    600
tactttgtga cttcacatac agcatttctca tacttagcta agcgatacgg attgactcag    660
ttaggtattg caggtgtctc aaccgagcaa gaacctagtg ctaaaaaatt agccgaaatt    720
caggagtttg tgaaaacata taagggttaag actatTTTTg ttgaagaagg agtctcacct    780
aaattagctc aagcagtagc ttcagctact cgagttaaaa ttgcaagttt aagtccttta    840
raagcagttc ccaaaaaaaa taaagattac ttagaaaatt tggaaactaa tcttaaggta    900
cttgtcaaat cgttaaatca atag                                     924
  
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<210> SEQ ID NO 65
 <211> LENGTH: 307
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae
 <220> FEATURE:
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(307)
 <223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 65

Met Lys Arg Ile Arg Lys Ser Leu Ile Phe Val Leu Gly Val Val Thr
 1 5 10 15
 Leu Ile Cys Leu Cys Ala Cys Thr Lys Gln Ser Gln Gln Lys Asn Gly
 20 25 30
 Leu Ser Val Val Thr Ser Phe Tyr Pro Val Tyr Ser Ile Thr Lys Ala
 35 40 45
 Val Ser Gly Asp Leu Asn Asp Ile Lys Met Ile Arg Ser Gln Ser Gly
 50 55 60
 Ile His Gly Phe Glu Pro Ser Ser Ser Asp Val Ala Ala Ile Tyr Asp
 65 70 75 80

-continued

Ala Asp Leu Phe Leu Tyr His Ser His Thr Leu Glu Ala Trp Ala Arg
85 90 95

Arg Leu Glu Pro Ser Leu His His Ser Lys Val Ser Val Ile Glu Ala
100 105 110

Ser Lys Gly Met Thr Leu Asp Lys Val His Gly Leu Glu Asp Val Glu
115 120 125

Ala Glu Lys Gly Val Asp Glu Ser Thr Leu Tyr Asp Pro His Thr Trp
130 135 140

Asn Asp Pro Val Lys Val Ser Glu Glu Ala Gln Leu Ile Ala Thr Gln
145 150 155 160

Leu Ala Lys Lys Asp Pro Lys Asn Ala Lys Val Tyr Gln Lys Asn Ala
165 170 175

Asp Gln Phe Ser Asp Lys Ala Met Ala Ile Ala Glu Lys Tyr Lys Pro
180 185 190

Lys Phe Lys Ala Ala Lys Ser Lys Tyr Phe Val Thr Ser His Thr Ala
195 200 205

Phe Ser Tyr Leu Ala Lys Arg Tyr Gly Leu Thr Gln Leu Gly Ile Ala
210 215 220

Gly Val Ser Thr Glu Gln Glu Pro Ser Ala Lys Lys Leu Ala Glu Ile
225 230 235 240

Gln Glu Phe Val Lys Thr Tyr Lys Val Lys Thr Ile Phe Val Glu Glu
245 250 255

Gly Val Ser Pro Lys Leu Ala Gln Ala Val Ala Ser Ala Thr Arg Val
260 265 270

Lys Ile Ala Ser Leu Ser Pro Leu Xaa Ala Val Pro Lys Asn Asn Lys
275 280 285

Asp Tyr Leu Glu Asn Leu Glu Thr Asn Leu Lys Val Leu Val Lys Ser
290 295 300

Leu Asn Gln
305

<210> SEQ ID NO 66

<211> LENGTH: 1134

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 66

```

atgcctaaga agaatcaga taccacagaa aaagaagaag ttgtcttaac ggaatggcaa      60
aagcgtaacc ttgaattttt aaaaaaacgc aaagaagatg aagaagaaca aaaacgtatt      120
aacgaaaaat tacgcttaga taaaagaagt aaattaaata tttcttctcc tgaagaacct      180
caaaatacta ctaaaattaa gaagcttcat tttccaaaga tttcaagacc taagattgaa      240
aagaaacaga aaaaagaaaa aatagtcaac agcttagcca aaactaatcg cattagaact      300
gcacctatat ttgtagtagc attcctagtc attttagttt ccgttttccct actaactcct      360
tttagtaagc aaaaaacaat aacagttagt ggaaatcagc atacacctga tgatattttg      420
atagagaaaa cgaatattca aaaaaacgat tatttctttt ctttaatttt taaacataaa      480
gctattgaac aacgttttagc tgcagaagat gtatgggtaa aaacagctca gatgacttat      540
caatttccca ataagtttca tattcaagtt caagaaaata agattattgc atatgcacat      600
acaaagcaag gatatcaacc tgtcttgaa actggaaaaa aggetgatcc tgtaaatagt      660
tcagagctac caaagcactt cttaacaatt aaccttgata aggaagatag tattaagcta      720
ttaattaaag atttaaaggc tttagacctt gatttaataa gtgagattca ggtgataagt      780

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ttagctgatt ctaaaacgac acctgacctc ctgctgttag atatgcacga tggaaatagt      840
attagaatac cattatctaa atttaaagaa agacttcctt tttacaaaca aattaagaag      900
aaccttaagg aaccttctat tggtgatatg gaagtgggag tttacacaac aacaaatacc      960
attgaatcaa ccctgtgtaa agcagaagat acaaaaaata aatcaactga taaaacacaa     1020
acacaaaatg gtcaggttgc ggaaaatagt caaggacaaa caaataactc aaatactaata     1080
caacaaggac aacagatagc aacagagcag gcacctaacc ctcaaatgt taat             1134

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<210> SEQ ID NO 67

<211> LENGTH: 378

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 67

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Met Pro Lys Lys Lys Ser Asp Thr Pro Glu Lys Glu Glu Val Val Leu
  1          5          10          15

Thr Glu Trp Gln Lys Arg Asn Leu Glu Phe Leu Lys Lys Arg Lys Glu
  20          25          30

Asp Glu Glu Glu Gln Lys Arg Ile Asn Glu Lys Leu Arg Leu Asp Lys
  35          40          45

Arg Ser Lys Leu Asn Ile Ser Ser Pro Glu Glu Pro Gln Asn Thr Thr
  50          55          60

Lys Ile Lys Lys Leu His Phe Pro Lys Ile Ser Arg Pro Lys Ile Glu
  65          70          75          80

Lys Lys Gln Lys Lys Glu Lys Ile Val Asn Ser Leu Ala Lys Thr Asn
  85          90          95

Arg Ile Arg Thr Ala Pro Ile Phe Val Val Ala Phe Leu Val Ile Leu
 100          105          110

Val Ser Val Phe Leu Leu Thr Pro Phe Ser Lys Gln Lys Thr Ile Thr
 115          120          125

Val Ser Gly Asn Gln His Thr Pro Asp Asp Ile Leu Ile Glu Lys Thr
 130          135          140

Asn Ile Gln Lys Asn Asp Tyr Phe Phe Ser Leu Ile Phe Lys His Lys
 145          150          155          160

Ala Ile Glu Gln Arg Leu Ala Ala Glu Asp Val Trp Val Lys Thr Ala
 165          170          175

Gln Met Thr Tyr Gln Phe Pro Asn Lys Phe His Ile Gln Val Gln Glu
 180          185          190

Asn Lys Ile Ile Ala Tyr Ala His Thr Lys Gln Gly Tyr Gln Pro Val
 195          200          205

Leu Glu Thr Gly Lys Lys Ala Asp Pro Val Asn Ser Ser Glu Leu Pro
 210          215          220

Lys His Phe Leu Thr Ile Asn Leu Asp Lys Glu Asp Ser Ile Lys Leu
 225          230          235          240

Leu Ile Lys Asp Leu Lys Ala Leu Asp Pro Asp Leu Ile Ser Glu Ile
 245          250          255

Gln Val Ile Ser Leu Ala Asp Ser Lys Thr Thr Pro Asp Leu Leu Leu
 260          265          270

Leu Asp Met His Asp Gly Asn Ser Ile Arg Ile Pro Leu Ser Lys Phe
 275          280          285

Lys Glu Arg Leu Pro Phe Tyr Lys Gln Ile Lys Lys Asn Leu Lys Glu
 290          295          300

Pro Ser Ile Val Asp Met Glu Val Gly Val Tyr Thr Thr Thr Asn Thr

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305	310	315	320
Ile Glu Ser Thr	Pro Val Lys Ala	Glu Asp Thr Lys Asn Lys Ser Thr	
	325	330	335
Asp Lys Thr	Gln Thr Gln Asn Gly	Gln Val Ala Glu Asn Ser Gln Gly	
	340	345	350
Gln Thr Asn Asn Ser Asn Thr Asn Gln Gln Gly	Gln Gln Ile Ala Thr		
	355	360	365
Glu Gln Ala Pro Asn Pro Gln Asn Val Asn			
	370	375	

<210> SEQ ID NO 68
 <211> LENGTH: 3699
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 68

gtggataaac atcactcaaa aaaggctatt ttaaagttaa cacttataac aactagtatt	60
ttattaatgc atagcaatca agtgaatgca gaggagcaag aattaaaaaa ccaagagcaa	120
tcacctgtaa ttgctaattgt tgctcaacag ccacgcgcat cggtaactac taatactgtt	180
gaaaaaacat ctgtaacagc tgcttctgct agtaatacag cgaaagaaat gggtgataca	240
tctgtaaaaa atgacaaaac agaagatgaa ttattagaag agttatctaa aaaccttgat	300
acgttctaatt tgggggctga tcttgaagaa gaatatccct ctaaaccaga gacaaccaac	360
aataaagaaa gcaatgtagt aacaaatgct tcaactgcaa tagcacagaa agttccctca	420
gcatatgaag aggtgaagcc agaaagcaag tcatcgcttg ctgttcttga tacatctaaa	480
ataacaaaat tacaagccat aacccaaaga ggaaagggaa atgtagtagc tattattgat	540
actggctttg atattaacca tgatatTTTT cgttttagata gcccaaaaga tgataagcac	600
agctttaaaa ctaagacaga atttgaggaa ttaaagcaa aacataatat cacttatggg	660
aaatgggtta acgataagat tgTTTTtgca cataactacg ccaacaatac agaaacgggtg	720
gctgatattg cagcagctat gaaagatggg tatgggtcag aagcaaagaa tatttcgcat	780
ggtagcacacg ttgctgggat tttttagagt aatagtaaac gtccagcaat caatgggtctt	840
cttttagaag gtgcacgccc aaatgctcaa gtcttattaa tgcgtattcc agataaaatt	900
gattcggaca aatttggtga agcatatgct aaagcaatca cagacgctgt taatctagga	960
gcaaaaacga ttaatatgag tattggaaaa acagctgatt ctttaattgc tctcaatgat	1020
aaagttaaat tagcacttaa attagcttct gagaaggcg tgacagttgt tgtggctgcc	1080
ggaaatgaag gcgcatttgg tatggattat agcaaaccat tatcaactaa tctgactac	1140
ggtagcggta atagtccagc tatttctgaa gatactttga gtgttgctag ctatgaatca	1200
cttaaaaacta tcagtggagt cgttgaaaca actattgaag gtaagttagt taagttgccg	1260
attgtgactt ctaaaccctt tgacaaaggt aaggcctacg atgtggttta tgccaattat	1320
ggtagcaaaa aagactttga aggtaaggac tttaaaggta agattgcatt aattgagcgt	1380
ggtaggtggac ttgattttat gactaaaatc actcatgcta caaatgcagg tgtgtgtgg	1440
atcgttatTT ttaacgatca agaaaaacgt ggaaatttTc taattcctta ccgtgaatta	1500
cctgtgggga ttattagtaa agtagatggc gagcgtataa aaaatacttc aagtcagtta	1560
acatttaacc agagttttga agtagttgat agccaagggt gtaatcgat gctggaacaa	1620
tcaagttggg gcgtgacagc tgaaggagca atcaagcctg atgtaacagc ttctggcttt	1680
gaaattttatt cttaaaccta taataatcaa taccaaacaa tgtctggtac aagtatggct	1740

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tcaccacatg ttgcaggatt aatgacaatg cttcaaagtc atttggctga gaaatataaa 1800
gggatgaatt tagattctaa aaaattgcta gaattgtcta aaaacatcct catgagctca 1860
gcaacagcat tatatagtga agaggataag gcgttttatt caccacgtca gcaagggtgca 1920
ggtgtagtgt atgctgaaaa agctatccaa gctcaatatt atattactgg aaacgatggc 1980
aaagctaaaa ttaatctcaa acgaatggga gataaatttg atatcacagt tacaattcat 2040
aaacttgtag aagggtgtcaa agaattgtat tatcaagcta atgtagcaac agaacaagta 2100
aataaaggta aatttgccct taaaccacaa gccttgctag atactaattg gcagaaagta 2160
attcttcgtg ataaagaaac acaagttcga tttactattg atgctagtca atttagtcag 2220
aaattaaaag aacagatggc aaatgggtat ttcttagaag gttttgtacg ttttaaagaa 2280
gccagggata gtaatcagga gttaatgagt attccttttg taggatttaa tgggtatttt 2340
gcgaacttac aagcacttga aacacogatt tataagacgc tttctaaagg tagtttctac 2400
tataaaccaa atgatacaac tcataaagac caattggagt acaatgaatc agctcctttt 2460
gaaagcaaca actatactgc cttgttaaca caatcagcgt cttggggcta tgttgattat 2520
gtcaaaaatg gtggggagtt agaattagca cgggagagtc caaaaagaat tatttttagga 2580
acttttgaga ataaggttga ggataaaaca attcatcttt tggaagaga tgcagcgaat 2640
aatccatatt ttgccatttc tccaaataaa gatggaaata gggacgaaat cactccccag 2700
gcaactttct taagaaatgt taaggatatt tctgctcaag ttctagatca aaatggaaat 2760
gttatttggc aaagtaaggt ttaccatct tatcgtaaaa atttccataa taatccaaag 2820
caaagtgatg gtcattatcg tatggatgct cttcagtggg gtggtttaga taaggatggc 2880
aaagttgtag cagatgggtt ttatacttat cgcttacgtt acacaccagt agcagaagga 2940
gcaaatagtc aggagtcaga ctttaaagta caagtaagta ctaagtcacc aaatcttcct 3000
tcacgagctc agtttgatga aactaatcga acattaagct tagccatgcc taaggaaagt 3060
agttatgttc ctacatatcg ttacaatta gttttatctc atgttgtaaa agatgaagaa 3120
tatgggggatg agacttctta ccattatttc catatagatc aagaaggtaa agtgacactt 3180
cctaaaaacgg ttaagatagg agagagttag gttgcggtag accctaaggc cttgacactt 3240
gttgtggaag ataaagctgg taatttcgca acggtaaaat tgtctgatct cttgaataag 3300
gcagtagtat cagagaaaga aaacgctata gtaatttcta acagtttcaa atattttgat 3360
aacttgaaaa aagaacctat gtttatttct aaaaaagaaa aagtagtaaa caagaatcta 3420
gaagaaataa tattagttaa gccgcaaact acagttacta ctcaatcatt gtctaaagaa 3480
ataactaaat caggaaatga gaaagtcctc acttctacaa acaataatag tagcagagta 3540
gctaagatca tatcacctaa acataacggg gattctgtta accatacctt acctagtaca 3600
tcagatagag caacgaatgg tctatttgtt ggtactttgg cattgttatc tagtttactt 3660
ctttatttga aacccaaaaa gactaaaaat aatagtaaa 3699

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<210> SEQ ID NO 69

<211> LENGTH: 1233

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 69

```

Val Asp Lys His His Ser Lys Lys Ala Ile Leu Lys Leu Thr Leu Ile
  1             5             10             15

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Thr Thr Ser Ile Leu Leu Met His Ser Asn Gln Val Asn Ala Glu Glu

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20					25					30					
Gln	Glu	Leu	Lys	Asn	Gln	Glu	Gln	Ser	Pro	Val	Ile	Ala	Asn	Val	Ala
		35					40					45			
Gln	Gln	Pro	Ser	Pro	Ser	Val	Thr	Thr	Asn	Thr	Val	Glu	Lys	Thr	Ser
		50				55					60				
Val	Thr	Ala	Ala	Ser	Ala	Ser	Asn	Thr	Ala	Lys	Glu	Met	Gly	Asp	Thr
65					70					75				80	
Ser	Val	Lys	Asn	Asp	Lys	Thr	Glu	Asp	Glu	Leu	Leu	Glu	Glu	Leu	Ser
			85						90					95	
Lys	Asn	Leu	Asp	Thr	Ser	Asn	Leu	Gly	Ala	Asp	Leu	Glu	Glu	Glu	Tyr
		100						105					110		
Pro	Ser	Lys	Pro	Glu	Thr	Thr	Asn	Asn	Lys	Glu	Ser	Asn	Val	Val	Thr
		115					120					125			
Asn	Ala	Ser	Thr	Ala	Ile	Ala	Gln	Lys	Val	Pro	Ser	Ala	Tyr	Glu	Glu
		130				135					140				
Val	Lys	Pro	Glu	Ser	Lys	Ser	Ser	Leu	Ala	Val	Leu	Asp	Thr	Ser	Lys
145					150					155					160
Ile	Thr	Lys	Leu	Gln	Ala	Ile	Thr	Gln	Arg	Gly	Lys	Gly	Asn	Val	Val
			165						170					175	
Ala	Ile	Ile	Asp	Thr	Gly	Phe	Asp	Ile	Asn	His	Asp	Ile	Phe	Arg	Leu
			180					185					190		
Asp	Ser	Pro	Lys	Asp	Asp	Lys	His	Ser	Phe	Lys	Thr	Lys	Thr	Glu	Phe
		195				200						205			
Glu	Glu	Leu	Lys	Ala	Lys	His	Asn	Ile	Thr	Tyr	Gly	Lys	Trp	Val	Asn
		210				215					220				
Asp	Lys	Ile	Val	Phe	Ala	His	Asn	Tyr	Ala	Asn	Asn	Thr	Glu	Thr	Val
225					230					235					240
Ala	Asp	Ile	Ala	Ala	Ala	Met	Lys	Asp	Gly	Tyr	Gly	Ser	Glu	Ala	Lys
			245						250					255	
Asn	Ile	Ser	His	Gly	Thr	His	Val	Ala	Gly	Ile	Phe	Val	Gly	Asn	Ser
		260					265						270		
Lys	Arg	Pro	Ala	Ile	Asn	Gly	Leu	Leu	Leu	Glu	Gly	Ala	Ala	Pro	Asn
		275				280						285			
Ala	Gln	Val	Leu	Leu	Met	Arg	Ile	Pro	Asp	Lys	Ile	Asp	Ser	Asp	Lys
		290				295					300				
Phe	Gly	Glu	Ala	Tyr	Ala	Lys	Ala	Ile	Thr	Asp	Ala	Val	Asn	Leu	Gly
305					310					315					320
Ala	Lys	Thr	Ile	Asn	Met	Ser	Ile	Gly	Lys	Thr	Ala	Asp	Ser	Leu	Ile
			325						330					335	
Ala	Leu	Asn	Asp	Lys	Val	Lys	Leu	Ala	Leu	Lys	Leu	Ala	Ser	Glu	Lys
		340					345						350		
Gly	Val	Ala	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Gly	Ala	Phe	Gly	Met
		355				360						365			
Asp	Tyr	Ser	Lys	Pro	Leu	Ser	Thr	Asn	Pro	Asp	Tyr	Gly	Thr	Val	Asn
		370				375					380				
Ser	Pro	Ala	Ile	Ser	Glu	Asp	Thr	Leu	Ser	Val	Ala	Ser	Tyr	Glu	Ser
385					390					395					400
Leu	Lys	Thr	Ile	Ser	Glu	Val	Val	Glu	Thr	Thr	Ile	Glu	Gly	Lys	Leu
			405						410					415	
Val	Lys	Leu	Pro	Ile	Val	Thr	Ser	Lys	Pro	Phe	Asp	Lys	Gly	Lys	Ala
			420					425					430		
Tyr	Asp	Val	Val	Tyr	Ala	Asn	Tyr	Gly	Ala	Lys	Lys	Asp	Phe	Glu	Gly
		435					440					445			

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Lys Asp Phe Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Gly Gly Leu
 450 455 460
 Asp Phe Met Thr Lys Ile Thr His Ala Thr Asn Ala Gly Val Val Gly
 465 470 475 480
 Ile Val Ile Phe Asn Asp Gln Glu Lys Arg Gly Asn Phe Leu Ile Pro
 485 490 495
 Tyr Arg Glu Leu Pro Val Gly Ile Ile Ser Lys Val Asp Gly Glu Arg
 500 505 510
 Ile Lys Asn Thr Ser Ser Gln Leu Thr Phe Asn Gln Ser Phe Glu Val
 515 520 525
 Val Asp Ser Gln Gly Gly Asn Arg Met Leu Glu Gln Ser Ser Trp Gly
 530 535 540
 Val Thr Ala Glu Gly Ala Ile Lys Pro Asp Val Thr Ala Ser Gly Phe
 545 550 555 560
 Glu Ile Tyr Ser Ser Thr Tyr Asn Asn Gln Tyr Gln Thr Met Ser Gly
 565 570 575
 Thr Ser Met Ala Ser Pro His Val Ala Gly Leu Met Thr Met Leu Gln
 580 585 590
 Ser His Leu Ala Glu Lys Tyr Lys Gly Met Asn Leu Asp Ser Lys Lys
 595 600 605
 Leu Leu Glu Leu Ser Lys Asn Ile Leu Met Ser Ser Ala Thr Ala Leu
 610 615 620
 Tyr Ser Glu Glu Asp Lys Ala Phe Tyr Ser Pro Arg Gln Gln Gly Ala
 625 630 635 640
 Gly Val Val Asp Ala Glu Lys Ala Ile Gln Ala Gln Tyr Tyr Ile Thr
 645 650 655
 Gly Asn Asp Gly Lys Ala Lys Ile Asn Leu Lys Arg Met Gly Asp Lys
 660 665 670
 Phe Asp Ile Thr Val Thr Ile His Lys Leu Val Glu Gly Val Lys Glu
 675 680 685
 Leu Tyr Tyr Gln Ala Asn Val Ala Thr Glu Gln Val Asn Lys Gly Lys
 690 695 700
 Phe Ala Leu Lys Pro Gln Ala Leu Leu Asp Thr Asn Trp Gln Lys Val
 705 710 715 720
 Ile Leu Arg Asp Lys Glu Thr Gln Val Arg Phe Thr Ile Asp Ala Ser
 725 730 735
 Gln Phe Ser Gln Lys Leu Lys Glu Gln Met Ala Asn Gly Tyr Phe Leu
 740 745 750
 Glu Gly Phe Val Arg Phe Lys Glu Ala Lys Asp Ser Asn Gln Glu Leu
 755 760 765
 Met Ser Ile Pro Phe Val Gly Phe Asn Gly Asp Phe Ala Asn Leu Gln
 770 775 780
 Ala Leu Glu Thr Pro Ile Tyr Lys Thr Leu Ser Lys Gly Ser Phe Tyr
 785 790 795 800
 Tyr Lys Pro Asn Asp Thr Thr His Lys Asp Gln Leu Glu Tyr Asn Glu
 805 810 815
 Ser Ala Pro Phe Glu Ser Asn Asn Tyr Thr Ala Leu Leu Thr Gln Ser
 820 825 830
 Ala Ser Trp Gly Tyr Val Asp Tyr Val Lys Asn Gly Gly Glu Leu Glu
 835 840 845
 Leu Ala Pro Glu Ser Pro Lys Arg Ile Ile Leu Gly Thr Phe Glu Asn
 850 855 860

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Lys Val Glu Asp Lys Thr Ile His Leu Leu Glu Arg Asp Ala Ala Asn
 865 870 875 880
 Asn Pro Tyr Phe Ala Ile Ser Pro Asn Lys Asp Gly Asn Arg Asp Glu
 885 890 895
 Ile Thr Pro Gln Ala Thr Phe Leu Arg Asn Val Lys Asp Ile Ser Ala
 900 905 910
 Gln Val Leu Asp Gln Asn Gly Asn Val Ile Trp Gln Ser Lys Val Leu
 915 920 925
 Pro Ser Tyr Arg Lys Asn Phe His Asn Asn Pro Lys Gln Ser Asp Gly
 930 935 940
 His Tyr Arg Met Asp Ala Leu Gln Trp Ser Gly Leu Asp Lys Asp Gly
 945 950 955 960
 Lys Val Val Ala Asp Gly Phe Tyr Thr Tyr Arg Leu Arg Tyr Thr Pro
 965 970 975
 Val Ala Glu Gly Ala Asn Ser Gln Glu Ser Asp Phe Lys Val Gln Val
 980 985 990
 Ser Thr Lys Ser Pro Asn Leu Pro Ser Arg Ala Gln Phe Asp Glu Thr
 995 1000 1005
 Asn Arg Thr Leu Ser Leu Ala Met Pro Lys Glu Ser Ser Tyr Val Pro
 1010 1015 1020
 Thr Tyr Arg Leu Gln Leu Val Leu Ser His Val Val Lys Asp Glu Glu
 1025 1030 1035 1040
 Tyr Gly Asp Glu Thr Ser Tyr His Tyr Phe His Ile Asp Gln Glu Gly
 1045 1050 1055
 Lys Val Thr Leu Pro Lys Thr Val Lys Ile Gly Glu Ser Glu Val Ala
 1060 1065 1070
 Val Asp Pro Lys Ala Leu Thr Leu Val Val Glu Asp Lys Ala Gly Asn
 1075 1080 1085
 Phe Ala Thr Val Lys Leu Ser Asp Leu Leu Asn Lys Ala Val Val Ser
 1090 1095 1100
 Glu Lys Glu Asn Ala Ile Val Ile Ser Asn Ser Phe Lys Tyr Phe Asp
 1105 1110 1115 1120
 Asn Leu Lys Lys Glu Pro Met Phe Ile Ser Lys Lys Glu Lys Val Val
 1125 1130 1135
 Asn Lys Asn Leu Glu Glu Ile Ile Leu Val Lys Pro Gln Thr Thr Val
 1140 1145 1150
 Thr Thr Gln Ser Leu Ser Lys Glu Ile Thr Lys Ser Gly Asn Glu Lys
 1155 1160 1165
 Val Leu Thr Ser Thr Asn Asn Asn Ser Ser Arg Val Ala Lys Ile Ile
 1170 1175 1180
 Ser Pro Lys His Asn Gly Asp Ser Val Asn His Thr Leu Pro Ser Thr
 1185 1190 1195 1200
 Ser Asp Arg Ala Thr Asn Gly Leu Phe Val Gly Thr Leu Ala Leu Leu
 1205 1210 1215
 Ser Ser Leu Leu Leu Tyr Leu Lys Pro Lys Lys Thr Lys Asn Asn Ser
 1220 1225 1230

Lys

<210> SEQ ID NO 70

<211> LENGTH: 1203

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 70

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Glu	Glu	Gln	Glu	Leu	Lys	Asn	Gln	Glu	Gln	Ser	Pro	Val	Ile	Ala	Asn	
1				5				10						15		
Val	Ala	Gln	Gln	Pro	Ser	Pro	Ser	Val	Thr	Thr	Asn	Thr	Val	Glu	Lys	
		20						25					30			
Thr	Ser	Val	Thr	Ala	Ala	Ser	Ala	Ser	Asn	Thr	Ala	Lys	Glu	Met	Gly	
	35						40					45				
Asp	Thr	Ser	Val	Lys	Asn	Asp	Lys	Thr	Glu	Asp	Glu	Leu	Leu	Glu	Glu	
50					55					60						
Leu	Ser	Lys	Asn	Leu	Asp	Thr	Ser	Asn	Leu	Gly	Ala	Asp	Leu	Glu	Glu	
65				70						75				80		
Glu	Tyr	Pro	Ser	Lys	Pro	Glu	Thr	Thr	Asn	Asn	Lys	Glu	Ser	Asn	Val	
			85					90						95		
Val	Thr	Asn	Ala	Ser	Thr	Ala	Ile	Ala	Gln	Lys	Val	Pro	Ser	Ala	Tyr	
		100						105					110			
Glu	Glu	Val	Lys	Pro	Glu	Ser	Lys	Ser	Ser	Leu	Ala	Val	Leu	Asp	Thr	
	115					120						125				
Ser	Lys	Ile	Thr	Lys	Leu	Gln	Ala	Ile	Thr	Gln	Arg	Gly	Lys	Gly	Asn	
130					135						140					
Val	Val	Ala	Ile	Ile	Asp	Thr	Gly	Phe	Asp	Ile	Asn	His	Asp	Ile	Phe	
145				150					155					160		
Arg	Leu	Asp	Ser	Pro	Lys	Asp	Asp	Lys	His	Ser	Phe	Lys	Thr	Lys	Thr	
			165					170						175		
Glu	Phe	Glu	Glu	Leu	Lys	Ala	Lys	His	Asn	Ile	Thr	Tyr	Gly	Lys	Trp	
	180						185						190			
Val	Asn	Asp	Lys	Ile	Val	Phe	Ala	His	Asn	Tyr	Ala	Asn	Asn	Thr	Glu	
	195					200						205				
Thr	Val	Ala	Asp	Ile	Ala	Ala	Ala	Met	Lys	Asp	Gly	Tyr	Gly	Ser	Glu	
210					215						220					
Ala	Lys	Asn	Ile	Ser	His	Gly	Thr	His	Val	Ala	Gly	Ile	Phe	Val	Gly	
225				230					235					240		
Asn	Ser	Lys	Arg	Pro	Ala	Ile	Asn	Gly	Leu	Leu	Leu	Glu	Gly	Ala	Ala	
			245					250						255		
Pro	Asn	Ala	Gln	Val	Leu	Leu	Met	Arg	Ile	Pro	Asp	Lys	Ile	Asp	Ser	
		260					265						270			
Asp	Lys	Phe	Gly	Glu	Ala	Tyr	Ala	Lys	Ala	Ile	Thr	Asp	Ala	Val	Asn	
	275					280						285				
Leu	Gly	Ala	Lys	Thr	Ile	Asn	Met	Ser	Ile	Gly	Lys	Thr	Ala	Asp	Ser	
290					295						300					
Leu	Ile	Ala	Leu	Asn	Asp	Lys	Val	Lys	Leu	Ala	Leu	Lys	Leu	Ala	Ser	
305				310					315					320		
Glu	Lys	Gly	Val	Ala	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Gly	Ala	Phe	
		325						330						335		
Gly	Met	Asp	Tyr	Ser	Lys	Pro	Leu	Ser	Thr	Asn	Pro	Asp	Tyr	Gly	Thr	
	340						345						350			
Val	Asn	Ser	Pro	Ala	Ile	Ser	Glu	Asp	Thr	Leu	Ser	Val	Ala	Ser	Tyr	
	355					360						365				
Glu	Ser	Leu	Lys	Thr	Ile	Ser	Glu	Val	Val	Glu	Thr	Thr	Ile	Glu	Gly	
370					375						380					
Lys	Leu	Val	Lys	Leu	Pro	Ile	Val	Thr	Ser	Lys	Pro	Phe	Asp	Lys	Gly	
385				390					395					400		
Lys	Ala	Tyr	Asp	Val	Val	Tyr	Ala	Asn	Tyr	Gly	Ala	Lys	Lys	Asp	Phe	
	405						410							415		
Glu	Gly	Lys	Asp	Phe	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Gly	Gly	

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420							425					430				
Gly	Leu	Asp	Phe	Met	Thr	Lys	Ile	Thr	His	Ala	Thr	Asn	Ala	Gly	Val	
		435					440					445				
Val	Gly	Ile	Val	Ile	Phe	Asn	Asp	Gln	Glu	Lys	Arg	Gly	Asn	Phe	Leu	
		450				455					460					
Ile	Pro	Tyr	Arg	Glu	Leu	Pro	Val	Gly	Ile	Ile	Ser	Lys	Val	Asp	Gly	
465					470					475				480		
Glu	Arg	Ile	Lys	Asn	Thr	Ser	Ser	Gln	Leu	Thr	Phe	Asn	Gln	Ser	Phe	
				485					490					495		
Glu	Val	Val	Asp	Ser	Gln	Gly	Gly	Asn	Arg	Met	Leu	Glu	Gln	Ser	Ser	
			500					505					510			
Trp	Gly	Val	Thr	Ala	Glu	Gly	Ala	Ile	Lys	Pro	Asp	Val	Thr	Ala	Ser	
		515					520					525				
Gly	Phe	Glu	Ile	Tyr	Ser	Ser	Thr	Tyr	Asn	Asn	Gln	Tyr	Gln	Thr	Met	
	530					535					540					
Ser	Gly	Thr	Ser	Met	Ala	Ser	Pro	His	Val	Ala	Gly	Leu	Met	Thr	Met	
545					550					555					560	
Leu	Gln	Ser	His	Leu	Ala	Glu	Lys	Tyr	Lys	Gly	Met	Asn	Leu	Asp	Ser	
				565					570					575		
Lys	Lys	Leu	Leu	Glu	Leu	Ser	Lys	Asn	Ile	Leu	Met	Ser	Ser	Ala	Thr	
			580					585					590			
Ala	Leu	Tyr	Ser	Glu	Glu	Asp	Lys	Ala	Phe	Tyr	Ser	Pro	Arg	Gln	Gln	
		595					600					605				
Gly	Ala	Gly	Val	Val	Asp	Ala	Glu	Lys	Ala	Ile	Gln	Ala	Gln	Tyr	Tyr	
	610					615					620					
Ile	Thr	Gly	Asn	Asp	Gly	Lys	Ala	Lys	Ile	Asn	Leu	Lys	Arg	Met	Gly	
625					630					635					640	
Asp	Lys	Phe	Asp	Ile	Thr	Val	Thr	Ile	His	Lys	Leu	Val	Glu	Gly	Val	
				645					650					655		
Lys	Glu	Leu	Tyr	Tyr	Gln	Ala	Asn	Val	Ala	Thr	Glu	Gln	Val	Asn	Lys	
			660				665						670			
Gly	Lys	Phe	Ala	Leu	Lys	Pro	Gln	Ala	Leu	Leu	Asp	Thr	Asn	Trp	Gln	
		675					680					685				
Lys	Val	Ile	Leu	Arg	Asp	Lys	Glu	Thr	Gln	Val	Arg	Phe	Thr	Ile	Asp	
	690					695					700					
Ala	Ser	Gln	Phe	Ser	Gln	Lys	Leu	Lys	Glu	Gln	Met	Ala	Asn	Gly	Tyr	
705					710					715					720	
Phe	Leu	Glu	Gly	Phe	Val	Arg	Phe	Lys	Glu	Ala	Lys	Asp	Ser	Asn	Gln	
				725					730					735		
Glu	Leu	Met	Ser	Ile	Pro	Phe	Val	Gly	Phe	Asn	Gly	Asp	Phe	Ala	Asn	
			740					745					750			
Leu	Gln	Ala	Leu	Glu	Thr	Pro	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Gly	Ser	
		755					760						765			
Phe	Tyr	Tyr	Lys	Pro	Asn	Asp	Thr	Thr	His	Lys	Asp	Gln	Leu	Glu	Tyr	
	770					775					780					
Asn	Glu	Ser	Ala	Pro	Phe	Glu	Ser	Asn	Asn	Tyr	Thr	Ala	Leu	Leu	Thr	
785					790					795					800	
Gln	Ser	Ala	Ser	Trp	Gly	Tyr	Val	Asp	Tyr	Val	Lys	Asn	Gly	Gly	Glu	
				805					810					815		
Leu	Glu	Leu	Ala	Pro	Glu	Ser	Pro	Lys	Arg	Ile	Ile	Leu	Gly	Thr	Phe	
			820					825					830			
Glu	Asn	Lys	Val	Glu	Asp	Lys	Thr	Ile	His	Leu	Leu	Glu	Arg	Asp	Ala	
		835					840					845				

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Ala Asn Asn Pro Tyr Phe Ala Ile Ser Pro Asn Lys Asp Gly Asn Arg
 850 855 860
 Asp Glu Ile Thr Pro Gln Ala Thr Phe Leu Arg Asn Val Lys Asp Ile
 865 870 875 880
 Ser Ala Gln Val Leu Asp Gln Asn Gly Asn Val Ile Trp Gln Ser Lys
 885 890 895
 Val Leu Pro Ser Tyr Arg Lys Asn Phe His Asn Asn Pro Lys Gln Ser
 900 905 910
 Asp Gly His Tyr Arg Met Asp Ala Leu Gln Trp Ser Gly Leu Asp Lys
 915 920 925
 Asp Gly Lys Val Val Ala Asp Gly Phe Tyr Thr Tyr Arg Leu Arg Tyr
 930 935 940
 Thr Pro Val Ala Glu Gly Ala Asn Ser Gln Glu Ser Asp Phe Lys Val
 945 950 955 960
 Gln Val Ser Thr Lys Ser Pro Asn Leu Pro Ser Arg Ala Gln Phe Asp
 965 970 975
 Glu Thr Asn Arg Thr Leu Ser Leu Ala Met Pro Lys Glu Ser Ser Tyr
 980 985 990
 Val Pro Thr Tyr Arg Leu Gln Leu Val Leu Ser His Val Val Lys Asp
 995 1000 1005
 Glu Glu Tyr Gly Asp Glu Thr Ser Tyr His Tyr Phe His Ile Asp Gln
 1010 1015 1020
 Glu Gly Lys Val Thr Leu Pro Lys Thr Val Lys Ile Gly Glu Ser Glu
 1025 1030 1035 1040
 Val Ala Val Asp Pro Lys Ala Leu Thr Leu Val Val Glu Asp Lys Ala
 1045 1050 1055
 Gly Asn Phe Ala Thr Val Lys Leu Ser Asp Leu Leu Asn Lys Ala Val
 1060 1065 1070
 Val Ser Glu Lys Glu Asn Ala Ile Val Ile Ser Asn Ser Phe Lys Tyr
 1075 1080 1085
 Phe Asp Asn Leu Lys Lys Glu Pro Met Phe Ile Ser Lys Lys Glu Lys
 1090 1095 1100
 Val Val Asn Lys Asn Leu Glu Glu Ile Ile Leu Val Lys Pro Gln Thr
 1105 1110 1115 1120
 Thr Val Thr Thr Gln Ser Leu Ser Lys Glu Ile Thr Lys Ser Gly Asn
 1125 1130 1135
 Glu Lys Val Leu Thr Ser Thr Asn Asn Asn Ser Ser Arg Val Ala Lys
 1140 1145 1150
 Ile Ile Ser Pro Lys His Asn Gly Asp Ser Val Asn His Thr Leu Pro
 1155 1160 1165
 Ser Thr Ser Asp Arg Ala Thr Asn Gly Leu Phe Val Gly Thr Leu Ala
 1170 1175 1180
 Leu Leu Ser Ser Leu Leu Leu Tyr Leu Lys Pro Lys Lys Thr Lys Asn
 1185 1190 1195 1200
 Asn Ser Lys

<210> SEQ ID NO 71

<211> LENGTH: 1196

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 71

Val Asp Lys His His Ser Lys Lys Ala Ile Leu Lys Leu Thr Leu Ile
 1 5 10 15

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Thr	Thr	Ser	Ile	Leu	Leu	Met	His	Ser	Asn	Gln	Val	Asn	Ala	Glu	Glu	
			20					25					30			
Gln	Glu	Leu	Lys	Asn	Gln	Glu	Gln	Ser	Pro	Val	Ile	Ala	Asn	Val	Ala	
		35					40					45				
Gln	Gln	Pro	Ser	Pro	Ser	Val	Thr	Thr	Asn	Thr	Val	Glu	Lys	Thr	Ser	
		50				55					60					
Val	Thr	Ala	Ala	Ser	Ala	Ser	Asn	Thr	Ala	Lys	Glu	Met	Gly	Asp	Thr	
65					70					75					80	
Ser	Val	Lys	Asn	Asp	Lys	Thr	Glu	Asp	Glu	Leu	Leu	Glu	Glu	Leu	Ser	
			85						90					95		
Lys	Asn	Leu	Asp	Thr	Ser	Asn	Leu	Gly	Ala	Asp	Leu	Glu	Glu	Glu	Tyr	
		100						105					110			
Pro	Ser	Lys	Pro	Glu	Thr	Thr	Asn	Asn	Lys	Glu	Ser	Asn	Val	Val	Thr	
		115					120					125				
Asn	Ala	Ser	Thr	Ala	Ile	Ala	Gln	Lys	Val	Pro	Ser	Ala	Tyr	Glu	Glu	
		130				135						140				
Val	Lys	Pro	Glu	Ser	Lys	Ser	Ser	Leu	Ala	Val	Leu	Asp	Thr	Ser	Lys	
145					150					155					160	
Ile	Thr	Lys	Leu	Gln	Ala	Ile	Thr	Gln	Arg	Gly	Lys	Gly	Asn	Val	Val	
			165					170						175		
Ala	Ile	Ile	Asp	Thr	Gly	Phe	Asp	Ile	Asn	His	Asp	Ile	Phe	Arg	Leu	
		180						185					190			
Asp	Ser	Pro	Lys	Asp	Asp	Lys	His	Ser	Phe	Lys	Thr	Lys	Thr	Glu	Phe	
		195					200					205				
Glu	Glu	Leu	Lys	Ala	Lys	His	Asn	Ile	Thr	Tyr	Gly	Lys	Trp	Val	Asn	
		210				215					220					
Asp	Lys	Ile	Val	Phe	Ala	His	Asn	Tyr	Ala	Asn	Asn	Thr	Glu	Thr	Val	
225					230					235					240	
Ala	Asp	Ile	Ala	Ala	Ala	Met	Lys	Asp	Gly	Tyr	Gly	Ser	Glu	Ala	Lys	
			245						250					255		
Asn	Ile	Ser	His	Gly	Thr	His	Val	Ala	Gly	Ile	Phe	Val	Gly	Asn	Ser	
		260						265					270			
Lys	Arg	Pro	Ala	Ile	Asn	Gly	Leu	Leu	Leu	Glu	Gly	Ala	Ala	Pro	Asn	
		275					280					285				
Ala	Gln	Val	Leu	Leu	Met	Arg	Ile	Pro	Asp	Lys	Ile	Asp	Ser	Asp	Lys	
		290				295					300					
Phe	Gly	Glu	Ala	Tyr	Ala	Lys	Ala	Ile	Thr	Asp	Ala	Val	Asn	Leu	Gly	
305					310					315					320	
Ala	Lys	Thr	Ile	Asn	Met	Ser	Ile	Gly	Lys	Thr	Ala	Asp	Ser	Leu	Ile	
			325						330					335		
Ala	Leu	Asn	Asp	Lys	Val	Lys	Leu	Ala	Leu	Lys	Leu	Ala	Ser	Glu	Lys	
		340						345					350			
Gly	Val	Ala	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Gly	Ala	Phe	Gly	Met	
		355					360					365				
Asp	Tyr	Ser	Lys	Pro	Leu	Ser	Thr	Asn	Pro	Asp	Tyr	Gly	Thr	Val	Asn	
		370				375						380				
Ser	Pro	Ala	Ile	Ser	Glu	Asp	Thr	Leu	Ser	Val	Ala	Ser	Tyr	Glu	Ser	
385					390					395					400	
Leu	Lys	Thr	Ile	Ser	Glu	Val	Val	Glu	Thr	Thr	Ile	Glu	Gly	Lys	Leu	
			405						410					415		
Val	Lys	Leu	Pro	Ile	Val	Thr	Ser	Lys	Pro	Phe	Asp	Lys	Gly	Lys	Ala	
			420					425					430			

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Tyr Asp Val Val Tyr Ala Asn Tyr Gly Ala Lys Lys Asp Phe Glu Gly
 435 440 445
 Lys Asp Phe Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Gly Gly Leu
 450 455 460
 Asp Phe Met Thr Lys Ile Thr His Ala Thr Asn Ala Gly Val Val Gly
 465 470 475 480
 Ile Val Ile Phe Asn Asp Gln Glu Lys Arg Gly Asn Phe Leu Ile Pro
 485 490 495
 Tyr Arg Glu Leu Pro Val Gly Ile Ile Ser Lys Val Asp Gly Glu Arg
 500 505 510
 Ile Lys Asn Thr Ser Ser Gln Leu Thr Phe Asn Gln Ser Phe Glu Val
 515 520 525
 Val Asp Ser Gln Gly Gly Asn Arg Met Leu Glu Gln Ser Ser Trp Gly
 530 535 540
 Val Thr Ala Glu Gly Ala Ile Lys Pro Asp Val Thr Ala Ser Gly Phe
 545 550 555 560
 Glu Ile Tyr Ser Ser Thr Tyr Asn Asn Gln Tyr Gln Thr Met Ser Gly
 565 570 575
 Thr Ser Met Ala Ser Pro His Val Ala Gly Leu Met Thr Met Leu Gln
 580 585 590
 Ser His Leu Ala Glu Lys Tyr Lys Gly Met Asn Leu Asp Ser Lys Lys
 595 600 605
 Leu Leu Glu Leu Ser Lys Asn Ile Leu Met Ser Ser Ala Thr Ala Leu
 610 615 620
 Tyr Ser Glu Glu Asp Lys Ala Phe Tyr Ser Pro Arg Gln Gln Gly Ala
 625 630 635 640
 Gly Val Val Asp Ala Glu Lys Ala Ile Gln Ala Gln Tyr Tyr Ile Thr
 645 650 655
 Gly Asn Asp Gly Lys Ala Lys Ile Asn Leu Lys Arg Met Gly Asp Lys
 660 665 670
 Phe Asp Ile Thr Val Thr Ile His Lys Leu Val Glu Gly Val Lys Glu
 675 680 685
 Leu Tyr Tyr Gln Ala Asn Val Ala Thr Glu Gln Val Asn Lys Gly Lys
 690 695 700
 Phe Ala Leu Lys Pro Gln Ala Leu Leu Asp Thr Asn Trp Gln Lys Val
 705 710 715 720
 Ile Leu Arg Asp Lys Glu Thr Gln Val Arg Phe Thr Ile Asp Ala Ser
 725 730 735
 Gln Phe Ser Gln Lys Leu Lys Glu Gln Met Ala Asn Gly Tyr Phe Leu
 740 745 750
 Glu Gly Phe Val Arg Phe Lys Glu Ala Lys Asp Ser Asn Gln Glu Leu
 755 760 765
 Met Ser Ile Pro Phe Val Gly Phe Asn Gly Asp Phe Ala Asn Leu Gln
 770 775 780
 Ala Leu Glu Thr Pro Ile Tyr Lys Thr Leu Ser Lys Gly Ser Phe Tyr
 785 790 795 800
 Tyr Lys Pro Asn Asp Thr Thr His Lys Asp Gln Leu Glu Tyr Asn Glu
 805 810 815
 Ser Ala Pro Phe Glu Ser Asn Asn Tyr Thr Ala Leu Leu Thr Gln Ser
 820 825 830
 Ala Ser Trp Gly Tyr Val Asp Tyr Val Lys Asn Gly Gly Glu Leu Glu
 835 840 845
 Leu Ala Pro Glu Ser Pro Lys Arg Ile Ile Leu Gly Thr Phe Glu Asn

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850	855	860
Lys Val Glu Asp Lys Thr Ile His Leu Leu Glu Arg Asp Ala Ala Asn 865 870 875 880		
Asn Pro Tyr Phe Ala Ile Ser Pro Asn Lys Asp Gly Asn Arg Asp Glu 885 890 895		
Ile Thr Pro Gln Ala Thr Phe Leu Arg Asn Val Lys Asp Ile Ser Ala 900 905 910		
Gln Val Leu Asp Gln Asn Gly Asn Val Ile Trp Gln Ser Lys Val Leu 915 920 925		
Pro Ser Tyr Arg Lys Asn Phe His Asn Asn Pro Lys Gln Ser Asp Gly 930 935 940		
His Tyr Arg Met Asp Ala Leu Gln Trp Ser Gly Leu Asp Lys Asp Gly 945 950 955 960		
Lys Val Val Ala Asp Gly Phe Tyr Thr Tyr Arg Leu Arg Tyr Thr Pro 965 970 975		
Val Ala Glu Gly Ala Asn Ser Gln Glu Ser Asp Phe Lys Val Gln Val 980 985 990		
Ser Thr Lys Ser Pro Asn Leu Pro Ser Arg Ala Gln Phe Asp Glu Thr 995 1000 1005		
Asn Arg Thr Leu Ser Leu Ala Met Pro Lys Glu Ser Ser Tyr Val Pro 1010 1015 1020		
Thr Tyr Arg Leu Gln Leu Val Leu Ser His Val Val Lys Asp Glu Glu 1025 1030 1035 1040		
Tyr Gly Asp Glu Thr Ser Tyr His Tyr Phe His Ile Asp Gln Glu Gly 1045 1050 1055		
Lys Val Thr Leu Pro Lys Thr Val Lys Ile Gly Glu Ser Glu Val Ala 1060 1065 1070		
Val Asp Pro Lys Ala Leu Thr Leu Val Val Glu Asp Lys Ala Gly Asn 1075 1080 1085		
Phe Ala Thr Val Lys Leu Ser Asp Leu Leu Asn Lys Ala Val Val Ser 1090 1095 1100		
Glu Lys Glu Asn Ala Ile Val Ile Ser Asn Ser Phe Lys Tyr Phe Asp 1105 1110 1115 1120		
Asn Leu Lys Lys Glu Pro Met Phe Ile Ser Lys Lys Glu Lys Val Val 1125 1130 1135		
Asn Lys Asn Leu Glu Glu Ile Ile Leu Val Lys Pro Gln Thr Thr Val 1140 1145 1150		
Thr Thr Gln Ser Leu Ser Lys Glu Ile Thr Lys Ser Gly Asn Glu Lys 1155 1160 1165		
Val Leu Thr Ser Thr Asn Asn Asn Ser Ser Arg Val Ala Lys Ile Ile 1170 1175 1180		
Ser Pro Lys His Asn Gly Asp Ser Val Asn His Thr 1185 1190 1195		

<210> SEQ ID NO 72

<211> LENGTH: 1166

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 72

Glu Glu Gln Glu Leu Lys Asn Gln Glu Gln Ser Pro Val Ile Ala Asn 1 5 10 15
Val Ala Gln Gln Pro Ser Pro Ser Val Thr Thr Asn Thr Val Glu Lys 20 25 30

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Thr	Ser	Val	Thr	Ala	Ala	Ser	Ala	Ser	Asn	Thr	Ala	Lys	Glu	Met	Gly
		35					40					45			
Asp	Thr	Ser	Val	Lys	Asn	Asp	Lys	Thr	Glu	Asp	Glu	Leu	Leu	Glu	Glu
	50				55					60					
Leu	Ser	Lys	Asn	Leu	Asp	Thr	Ser	Asn	Leu	Gly	Ala	Asp	Leu	Glu	Glu
65				70						75				80	
Glu	Tyr	Pro	Ser	Lys	Pro	Glu	Thr	Thr	Asn	Asn	Lys	Glu	Ser	Asn	Val
			85						90					95	
Val	Thr	Asn	Ala	Ser	Thr	Ala	Ile	Ala	Gln	Lys	Val	Pro	Ser	Ala	Tyr
			100					105					110		
Glu	Glu	Val	Lys	Pro	Glu	Ser	Lys	Ser	Ser	Leu	Ala	Val	Leu	Asp	Thr
		115					120					125			
Ser	Lys	Ile	Thr	Lys	Leu	Gln	Ala	Ile	Thr	Gln	Arg	Gly	Lys	Gly	Asn
	130					135					140				
Val	Val	Ala	Ile	Ile	Asp	Thr	Gly	Phe	Asp	Ile	Asn	His	Asp	Ile	Phe
145					150					155					160
Arg	Leu	Asp	Ser	Pro	Lys	Asp	Asp	Lys	His	Ser	Phe	Lys	Thr	Lys	Thr
			165						170					175	
Glu	Phe	Glu	Glu	Leu	Lys	Ala	Lys	His	Asn	Ile	Thr	Tyr	Gly	Lys	Trp
		180						185					190		
Val	Asn	Asp	Lys	Ile	Val	Phe	Ala	His	Asn	Tyr	Ala	Asn	Asn	Thr	Glu
	195						200					205			
Thr	Val	Ala	Asp	Ile	Ala	Ala	Ala	Met	Lys	Asp	Gly	Tyr	Gly	Ser	Glu
	210					215					220				
Ala	Lys	Asn	Ile	Ser	His	Gly	Thr	His	Val	Ala	Gly	Ile	Phe	Val	Gly
225					230					235					240
Asn	Ser	Lys	Arg	Pro	Ala	Ile	Asn	Gly	Leu	Leu	Leu	Glu	Gly	Ala	Ala
			245						250					255	
Pro	Asn	Ala	Gln	Val	Leu	Leu	Met	Arg	Ile	Pro	Asp	Lys	Ile	Asp	Ser
			260					265					270		
Asp	Lys	Phe	Gly	Glu	Ala	Tyr	Ala	Lys	Ala	Ile	Thr	Asp	Ala	Val	Asn
		275					280					285			
Leu	Gly	Ala	Lys	Thr	Ile	Asn	Met	Ser	Ile	Gly	Lys	Thr	Ala	Asp	Ser
	290					295					300				
Leu	Ile	Ala	Leu	Asn	Asp	Lys	Val	Lys	Leu	Ala	Leu	Lys	Leu	Ala	Ser
305				310						315					320
Glu	Lys	Gly	Val	Ala	Val	Val	Val	Ala	Ala	Gly	Asn	Glu	Gly	Ala	Phe
			325						330					335	
Gly	Met	Asp	Tyr	Ser	Lys	Pro	Leu	Ser	Thr	Asn	Pro	Asp	Tyr	Gly	Thr
		340						345					350		
Val	Asn	Ser	Pro	Ala	Ile	Ser	Glu	Asp	Thr	Leu	Ser	Val	Ala	Ser	Tyr
		355					360					365			
Glu	Ser	Leu	Lys	Thr	Ile	Ser	Glu	Val	Val	Glu	Thr	Thr	Ile	Glu	Gly
	370					375					380				
Lys	Leu	Val	Lys	Leu	Pro	Ile	Val	Thr	Ser	Lys	Pro	Phe	Asp	Lys	Gly
385				390						395					400
Lys	Ala	Tyr	Asp	Val	Val	Tyr	Ala	Asn	Tyr	Gly	Ala	Lys	Lys	Asp	Phe
			405						410					415	
Glu	Gly	Lys	Asp	Phe	Lys	Gly	Lys	Ile	Ala	Leu	Ile	Glu	Arg	Gly	Gly
		420					425					430			
Gly	Leu	Asp	Phe	Met	Thr	Lys	Ile	Thr	His	Ala	Thr	Asn	Ala	Gly	Val
	435						440					445			
Val	Gly	Ile	Val	Ile	Phe	Asn	Asp	Gln	Glu	Lys	Arg	Gly	Asn	Phe	Leu

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450	455	460
Ile Pro Tyr Arg Glu Leu Pro Val Gly Ile Ile Ser Lys Val Asp Gly		
465	470	475 480
Glu Arg Ile Lys Asn Thr Ser Ser Gln Leu Thr Phe Asn Gln Ser Phe		
	485	490 495
Glu Val Val Asp Ser Gln Gly Gly Asn Arg Met Leu Glu Gln Ser Ser		
	500	505 510
Trp Gly Val Thr Ala Glu Gly Ala Ile Lys Pro Asp Val Thr Ala Ser		
	515	520 525
Gly Phe Glu Ile Tyr Ser Ser Thr Tyr Asn Asn Gln Tyr Gln Thr Met		
	530	535 540
Ser Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Leu Met Thr Met		
545	550	555 560
Leu Gln Ser His Leu Ala Glu Lys Tyr Lys Gly Met Asn Leu Asp Ser		
	565	570 575
Lys Lys Leu Leu Glu Leu Ser Lys Asn Ile Leu Met Ser Ser Ala Thr		
	580	585 590
Ala Leu Tyr Ser Glu Glu Asp Lys Ala Phe Tyr Ser Pro Arg Gln Gln		
	595	600 605
Gly Ala Gly Val Val Asp Ala Glu Lys Ala Ile Gln Ala Gln Tyr Tyr		
	610	615 620
Ile Thr Gly Asn Asp Gly Lys Ala Lys Ile Asn Leu Lys Arg Met Gly		
625	630	635 640
Asp Lys Phe Asp Ile Thr Val Thr Ile His Lys Leu Val Glu Gly Val		
	645	650 655
Lys Glu Leu Tyr Tyr Gln Ala Asn Val Ala Thr Glu Gln Val Asn Lys		
	660	665 670
Gly Lys Phe Ala Leu Lys Pro Gln Ala Leu Leu Asp Thr Asn Trp Gln		
	675	680 685
Lys Val Ile Leu Arg Asp Lys Glu Thr Gln Val Arg Phe Thr Ile Asp		
	690	695 700
Ala Ser Gln Phe Ser Gln Lys Leu Lys Glu Gln Met Ala Asn Gly Tyr		
705	710	715 720
Phe Leu Glu Gly Phe Val Arg Phe Lys Glu Ala Lys Asp Ser Asn Gln		
	725	730 735
Glu Leu Met Ser Ile Pro Phe Val Gly Phe Asn Gly Asp Phe Ala Asn		
	740	745 750
Leu Gln Ala Leu Glu Thr Pro Ile Tyr Lys Thr Leu Ser Lys Gly Ser		
	755	760 765
Phe Tyr Tyr Lys Pro Asn Asp Thr Thr His Lys Asp Gln Leu Glu Tyr		
	770	775 780
Asn Glu Ser Ala Pro Phe Glu Ser Asn Asn Tyr Thr Ala Leu Leu Thr		
785	790	795 800
Gln Ser Ala Ser Trp Gly Tyr Val Asp Tyr Val Lys Asn Gly Gly Glu		
	805	810 815
Leu Glu Leu Ala Pro Glu Ser Pro Lys Arg Ile Ile Leu Gly Thr Phe		
	820	825 830
Glu Asn Lys Val Glu Asp Lys Thr Ile His Leu Leu Glu Arg Asp Ala		
	835	840 845
Ala Asn Asn Pro Tyr Phe Ala Ile Ser Pro Asn Lys Asp Gly Asn Arg		
	850	855 860
Asp Glu Ile Thr Pro Gln Ala Thr Phe Leu Arg Asn Val Lys Asp Ile		
865	870	875 880

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Ser Ala Gln Val Leu Asp Gln Asn Gly Asn Val Ile Trp Gln Ser Lys
 885 890 895
 Val Leu Pro Ser Tyr Arg Lys Asn Phe His Asn Asn Pro Lys Gln Ser
 900 905 910
 Asp Gly His Tyr Arg Met Asp Ala Leu Gln Trp Ser Gly Leu Asp Lys
 915 920 925
 Asp Gly Lys Val Val Ala Asp Gly Phe Tyr Thr Tyr Arg Leu Arg Tyr
 930 935 940
 Thr Pro Val Ala Glu Gly Ala Asn Ser Gln Glu Ser Asp Phe Lys Val
 945 950 955 960
 Gln Val Ser Thr Lys Ser Pro Asn Leu Pro Ser Arg Ala Gln Phe Asp
 965 970 975
 Glu Thr Asn Arg Thr Leu Ser Leu Ala Met Pro Lys Glu Ser Ser Tyr
 980 985 990
 Val Pro Thr Tyr Arg Leu Gln Leu Val Leu Ser His Val Val Lys Asp
 995 1000 1005
 Glu Glu Tyr Gly Asp Glu Thr Ser Tyr His Tyr Phe His Ile Asp Gln
 1010 1015 1020
 Glu Gly Lys Val Thr Leu Pro Lys Thr Val Lys Ile Gly Glu Ser Glu
 1025 1030 1035 1040
 Val Ala Val Asp Pro Lys Ala Leu Thr Leu Val Val Glu Asp Lys Ala
 1045 1050 1055
 Gly Asn Phe Ala Thr Val Lys Leu Ser Asp Leu Leu Asn Lys Ala Val
 1060 1065 1070
 Val Ser Glu Lys Glu Asn Ala Ile Val Ile Ser Asn Ser Phe Lys Tyr
 1075 1080 1085
 Phe Asp Asn Leu Lys Lys Glu Pro Met Phe Ile Ser Lys Lys Glu Lys
 1090 1095 1100
 Val Val Asn Lys Asn Leu Glu Glu Ile Ile Leu Val Lys Pro Gln Thr
 1105 1110 1115 1120
 Thr Val Thr Thr Gln Ser Leu Ser Lys Glu Ile Thr Lys Ser Gly Asn
 1125 1130 1135
 Glu Lys Val Leu Thr Ser Thr Asn Asn Asn Ser Ser Arg Val Ala Lys
 1140 1145 1150
 Ile Ile Ser Pro Lys His Asn Gly Asp Ser Val Asn His Thr
 1155 1160 1165

<210> SEQ ID NO 73

<211> LENGTH: 2040

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 73

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atgaaacgta aatactttat tcttaatacg gtgacgggtt taacgttagc tgctgcaatg      60
aatactagca gtatctatgc taatagtact gagacaagtg cttcagtagt tcctactaca      120
aatactatcg ttcaactaa tgacagtaat cctaccgcaa aatttgtatc agaatcagga      180
caatctgtaa taggtcaagt aaaaccagat aattctgctg cgcttacaac agttgacacg      240
cctcatcata tttcagctcc agatgcttta aaaacaactc aatcaagtcc tgctggtgag      300
agtacttcta ctaagttaac tgaagagact tacaacaaa aagatggtca agatttagcc      360
aacatggtga gaagtgtgca agttactagt gaggaactcg ttaatatggc atacgatatt      420
attgctaag aaaccaccatc tttaaatgca gtcattacta ctagacgcc aagaagctatt      480

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gaagaggcta gaaaacttaa agataccaat cagccgtttt taggtgttcc cttgttagtc 540
aaggggttag ggcacagtat taaaggtggt gaaaccaata atggcttgat ctatgcagat 600
ggaaaaatta gcacatttga cagtagctat gtcaaaaaat ataaagattt aggatttatt 660
attttaggac aaacgaactt tccagagtat ggggtggcgt atataacaga ttctaaatta 720
tacggctctaa cgcataatcc ttgggatctt gctcataatg ctgggtggctc ttctggtgga 780
agtgcagcag ccattgctag cggaatgacg ccaattgcta gcggtagtga tgctggtggt 840
tctatccgta ttccatcttc ttggacgggc ttggtaggtt taaaaccaac aagaggattg 900
gtgagtaaat aaaagccaga ttcgtatagt acagcagttc attttccatt aactaagtca 960
tctagagacg cagaaacatt attaacttat ctaaagaaaa gcgatcaaac gctagtatca 1020
gttaatgatt taaaatcttt accaattgct tatactttga aatcaccaat gggaacagaa 1080
gttagtcaag atgctaaaaa cgctattatg gacaacgtca cattcttaag aaaacaagga 1140
ttcaaagtaa cagagataga cttaccaatt gatggtagag cattaatgcg tgattattca 1200
accttggcta ttggcatggg aggagctttt tcaacaattg aaaagactt aaaaaacat 1260
ggttttacta aagaagacgt tgatcctatt acttgggcag ttcattgtat ttatcaaaat 1320
tcagataagg ctgaacttaa gaaatctatt atggaagccc aaaaacatat ggatgattat 1380
cgtaaggcaa tggagaagct tcacaagcaa tttcctattt tcttatcgcc aacgaccgca 1440
agtttagccc ctctaatac agatccatat gtaacagagg aagataaaag agcgatttat 1500
aatatggaaa acttgagcca agaagaaaga attgctctct ttaatcgcca gtgggagcct 1560
atgttgcgta gaacaccttt tacacaaatt gctaatatga caggactccc agctatcagt 1620
atcccagctt acttatctga gtctggttta cccataggga cgatgttaat ggcagggtgca 1680
aactatgata tggattaat taaatttgca actttctttg aaaaacatca tggttttaat 1740
gttaaatggc aaagaataat agataaagaa gtgaaaccat ctactggcct aatacagcct 1800
actaactccc tctttaaagc tcattcatca ttagtaaatt tagaagaaaa ttcacaagtt 1860
actcaagtat ctatctctaa aaaatggatg aaatcgtctg ttaaaaataa accatccgta 1920
atggcatatc aaaaagcact tcctaaaaca ggtgatacag aatcaagcct atctccagtt 1980
ttagtagtaa cccttttatt agcttgtttt agctttgtaa caaaaaagaa tcagaaaagt 2040

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<210> SEQ ID NO 74

<211> LENGTH: 680

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 74

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Met Lys Arg Lys Tyr Phe Ile Leu Asn Thr Val Thr Val Leu Thr Leu
 1             5             10             15

Ala Ala Ala Met Asn Thr Ser Ser Ile Tyr Ala Asn Ser Thr Glu Thr
 20             25             30

Ser Ala Ser Val Val Pro Thr Thr Asn Thr Ile Val Gln Thr Asn Asp
 35             40             45

Ser Asn Pro Thr Ala Lys Phe Val Ser Glu Ser Gly Gln Ser Val Ile
 50             55             60

Gly Gln Val Lys Pro Asp Asn Ser Ala Ala Leu Thr Thr Val Asp Thr
 65             70             75             80

Pro His His Ile Ser Ala Pro Asp Ala Leu Lys Thr Thr Gln Ser Ser
 85             90             95

Pro Val Val Glu Ser Thr Ser Thr Lys Leu Thr Glu Glu Thr Tyr Lys

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100							105					110				
Gln	Lys	Asp	Gly	Gln	Asp	Leu	Ala	Asn	Met	Val	Arg	Ser	Gly	Gln	Val	
		115					120					125				
Thr	Ser	Glu	Glu	Leu	Val	Asn	Met	Ala	Tyr	Asp	Ile	Ile	Ala	Lys	Glu	
		130					135				140					
Asn	Pro	Ser	Leu	Asn	Ala	Val	Ile	Thr	Thr	Arg	Arg	Gln	Glu	Ala	Ile	
145					150					155					160	
Glu	Glu	Ala	Arg	Lys	Leu	Lys	Asp	Thr	Asn	Gln	Pro	Phe	Leu	Gly	Val	
				165					170					175		
Pro	Leu	Leu	Val	Lys	Gly	Leu	Gly	His	Ser	Ile	Lys	Gly	Gly	Glu	Thr	
			180					185					190			
Asn	Asn	Gly	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Ile	Ser	Thr	Phe	Asp	Ser	
		195					200					205				
Ser	Tyr	Val	Lys	Lys	Tyr	Lys	Asp	Leu	Gly	Phe	Ile	Ile	Leu	Gly	Gln	
		210					215					220				
Thr	Asn	Phe	Pro	Glu	Tyr	Gly	Trp	Arg	Asn	Ile	Thr	Asp	Ser	Lys	Leu	
225					230					235					240	
Tyr	Gly	Leu	Thr	His	Asn	Pro	Trp	Asp	Leu	Ala	His	Asn	Ala	Gly	Gly	
				245					250					255		
Ser	Ser	Gly	Gly	Ser	Ala	Ala	Ala	Ile	Ala	Ser	Gly	Met	Thr	Pro	Ile	
			260					265					270			
Ala	Ser	Gly	Ser	Asp	Ala	Gly	Gly	Ser	Ile	Arg	Ile	Pro	Ser	Ser	Trp	
		275					280					285				
Thr	Gly	Leu	Val	Gly	Leu	Lys	Pro	Thr	Arg	Gly	Leu	Val	Ser	Asn	Glu	
		290				295					300					
Lys	Pro	Asp	Ser	Tyr	Ser	Thr	Ala	Val	His	Phe	Pro	Leu	Thr	Lys	Ser	
305					310					315					320	
Ser	Arg	Asp	Ala	Glu	Thr	Leu	Leu	Thr	Tyr	Leu	Lys	Lys	Ser	Asp	Gln	
			325						330					335		
Thr	Leu	Val	Ser	Val	Asn	Asp	Leu	Lys	Ser	Leu	Pro	Ile	Ala	Tyr	Thr	
			340					345					350			
Leu	Lys	Ser	Pro	Met	Gly	Thr	Glu	Val	Ser	Gln	Asp	Ala	Lys	Asn	Ala	
		355					360					365				
Ile	Met	Asp	Asn	Val	Thr	Phe	Leu	Arg	Lys	Gln	Gly	Phe	Lys	Val	Thr	
		370				375					380					
Glu	Ile	Asp	Leu	Pro	Ile	Asp	Gly	Arg	Ala	Leu	Met	Arg	Asp	Tyr	Ser	
385					390					395					400	
Thr	Leu	Ala	Ile	Gly	Met	Gly	Gly	Ala	Phe	Ser	Thr	Ile	Glu	Lys	Asp	
			405						410					415		
Leu	Lys	Lys	His	Gly	Phe	Thr	Lys	Glu	Asp	Val	Asp	Pro	Ile	Thr	Trp	
			420						425				430			
Ala	Val	His	Val	Ile	Tyr	Gln	Asn	Ser	Asp	Lys	Ala	Glu	Leu	Lys	Lys	
		435					440					445				
Ser	Ile	Met	Glu	Ala	Gln	Lys	His	Met	Asp	Asp	Tyr	Arg	Lys	Ala	Met	
		450					455					460				
Glu	Lys	Leu	His	Lys	Gln	Phe	Pro	Ile	Phe	Leu	Ser	Pro	Thr	Thr	Ala	
465					470					475					480	
Ser	Leu	Ala	Pro	Leu	Asn	Thr	Asp	Pro	Tyr	Val	Thr	Glu	Glu	Asp	Lys	
				485					490					495		
Arg	Ala	Ile	Tyr	Asn	Met	Glu	Asn	Leu	Ser	Gln	Glu	Glu	Arg	Ile	Ala	
			500					505					510			
Leu	Phe	Asn	Arg	Gln	Trp	Glu	Pro	Met	Leu	Arg	Arg	Thr	Pro	Phe	Thr	
		515					520					525				

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Gln Ile Ala Asn Met Thr Gly Leu Pro Ala Ile Ser Ile Pro Thr Tyr
530 535 540

Leu Ser Glu Ser Gly Leu Pro Ile Gly Thr Met Leu Met Ala Gly Ala
545 550 555 560

Asn Tyr Asp Met Val Leu Ile Lys Phe Ala Thr Phe Phe Glu Lys His
565 570 575

His Gly Phe Asn Val Lys Trp Gln Arg Ile Ile Asp Lys Glu Val Lys
580 585 590

Pro Ser Thr Gly Leu Ile Gln Pro Thr Asn Ser Leu Phe Lys Ala His
595 600 605

Ser Ser Leu Val Asn Leu Glu Glu Asn Ser Gln Val Thr Gln Val Ser
610 615 620

Ile Ser Lys Lys Trp Met Lys Ser Ser Val Lys Asn Lys Pro Ser Val
625 630 635 640

Met Ala Tyr Gln Lys Ala Leu Pro Lys Thr Gly Asp Thr Glu Ser Ser
645 650 655

Leu Ser Pro Val Leu Val Val Thr Leu Leu Leu Ala Cys Phe Ser Phe
660 665 670

Val Thr Lys Lys Asn Gln Lys Ser
675 680

<210> SEQ ID NO 75

<211> LENGTH: 642

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 75

Thr Thr Asn Thr Ile Val Gln Thr Asn Asp Ser Asn Pro Thr Ala Lys
1 5 10 15

Phe Val Ser Glu Ser Gly Gln Ser Val Ile Gly Gln Val Lys Pro Asp
20 25 30

Asn Ser Ala Ala Leu Thr Thr Val Asp Thr Pro His His Ile Ser Ala
35 40 45

Pro Asp Ala Leu Lys Thr Thr Gln Ser Ser Pro Val Val Glu Ser Thr
50 55 60

Ser Thr Lys Leu Thr Glu Glu Thr Tyr Lys Gln Lys Asp Gly Gln Asp
65 70 75 80

Leu Ala Asn Met Val Arg Ser Gly Gln Val Thr Ser Glu Glu Leu Val
85 90 95

Asn Met Ala Tyr Asp Ile Ile Ala Lys Glu Asn Pro Ser Leu Asn Ala
100 105 110

Val Ile Thr Thr Arg Arg Gln Glu Ala Ile Glu Glu Ala Arg Lys Leu
115 120 125

Lys Asp Thr Asn Gln Pro Phe Leu Gly Val Pro Leu Leu Val Lys Gly
130 135 140

Leu Gly His Ser Ile Lys Gly Gly Glu Thr Asn Asn Gly Leu Ile Tyr
145 150 155 160

Ala Asp Gly Lys Ile Ser Thr Phe Asp Ser Ser Tyr Val Lys Lys Tyr
165 170 175

Lys Asp Leu Gly Phe Ile Ile Leu Gly Gln Thr Asn Phe Pro Glu Tyr
180 185 190

Gly Trp Arg Asn Ile Thr Asp Ser Lys Leu Tyr Gly Leu Thr His Asn
195 200 205

Pro Trp Asp Leu Ala His Asn Ala Gly Gly Ser Ser Gly Gly Ser Ala

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210	215	220
Ala Ala Ile Ala Ser Gly Met Thr Pro Ile Ala Ser Gly Ser Asp Ala		
225	230	235 240
Gly Gly Ser Ile Arg Ile Pro Ser Ser Trp Thr Gly Leu Val Gly Leu		
	245	250 255
Lys Pro Thr Arg Gly Leu Val Ser Asn Glu Lys Pro Asp Ser Tyr Ser		
	260	265 270
Thr Ala Val His Phe Pro Leu Thr Lys Ser Ser Arg Asp Ala Glu Thr		
	275	280 285
Leu Leu Thr Tyr Leu Lys Lys Ser Asp Gln Thr Leu Val Ser Val Asn		
	290	295 300
Asp Leu Lys Ser Leu Pro Ile Ala Tyr Thr Leu Lys Ser Pro Met Gly		
305	310	315 320
Thr Glu Val Ser Gln Asp Ala Lys Asn Ala Ile Met Asp Asn Val Thr		
	325	330 335
Phe Leu Arg Lys Gln Gly Phe Lys Val Thr Glu Ile Asp Leu Pro Ile		
	340	345 350
Asp Gly Arg Ala Leu Met Arg Asp Tyr Ser Thr Leu Ala Ile Gly Met		
	355	360 365
Gly Gly Ala Phe Ser Thr Ile Glu Lys Asp Leu Lys Lys His Gly Phe		
	370	375 380
Thr Lys Glu Asp Val Asp Pro Ile Thr Trp Ala Val His Val Ile Tyr		
385	390	395 400
Gln Asn Ser Asp Lys Ala Glu Leu Lys Lys Ser Ile Met Glu Ala Gln		
	405	410 415
Lys His Met Asp Asp Tyr Arg Lys Ala Met Glu Lys Leu His Lys Gln		
	420	425 430
Phe Pro Ile Phe Leu Ser Pro Thr Thr Ala Ser Leu Ala Pro Leu Asn		
	435	440 445
Thr Asp Pro Tyr Val Thr Glu Glu Asp Lys Arg Ala Ile Tyr Asn Met		
	450	455 460
Glu Asn Leu Ser Gln Glu Glu Arg Ile Ala Leu Phe Asn Arg Gln Trp		
465	470	475 480
Glu Pro Met Leu Arg Arg Thr Pro Phe Thr Gln Ile Ala Asn Met Thr		
	485	490 495
Gly Leu Pro Ala Ile Ser Ile Pro Thr Tyr Leu Ser Glu Ser Gly Leu		
	500	505 510
Pro Ile Gly Thr Met Leu Met Ala Gly Ala Asn Tyr Asp Met Val Leu		
	515	520 525
Ile Lys Phe Ala Thr Phe Phe Glu Lys His His Gly Phe Asn Val Lys		
	530	535 540
Trp Gln Arg Ile Ile Asp Lys Glu Val Lys Pro Ser Thr Gly Leu Ile		
545	550	555 560
Gln Pro Thr Asn Ser Leu Phe Lys Ala His Ser Ser Leu Val Asn Leu		
	565	570 575
Glu Glu Asn Ser Gln Val Thr Gln Val Ser Ile Ser Lys Lys Trp Met		
	580	585 590
Lys Ser Ser Val Lys Asn Lys Pro Ser Val Met Ala Tyr Gln Lys Ala		
	595	600 605
Leu Pro Lys Thr Gly Asp Thr Glu Ser Ser Leu Ser Pro Val Leu Val		
	610	615 620
Val Thr Leu Leu Leu Ala Cys Phe Ser Phe Val Thr Lys Lys Asn Gln		
625	630	635 640

-continued

Lys Ser

<210> SEQ ID NO 76

<211> LENGTH: 637

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 76

```

Met Lys Arg Lys Tyr Phe Ile Leu Asn Thr Val Thr Val Leu Thr Leu
 1         5         10        15
Ala Ala Ala Met Asn Thr Ser Ser Ile Tyr Ala Asn Ser Thr Glu Thr
 20        25        30
Ser Ala Ser Val Val Pro Thr Thr Asn Thr Ile Val Gln Thr Asn Asp
 35        40        45
Ser Asn Pro Thr Ala Lys Phe Val Ser Glu Ser Gly Gln Ser Val Ile
 50        55        60
Gly Gln Val Lys Pro Asp Asn Ser Ala Ala Leu Thr Thr Val Asp Thr
 65        70        75        80
Pro His His Ile Ser Ala Pro Asp Ala Leu Lys Thr Thr Gln Ser Ser
 85        90        95
Pro Val Val Glu Ser Thr Ser Thr Lys Leu Thr Glu Glu Thr Tyr Lys
100       105       110
Gln Lys Asp Gly Gln Asp Leu Ala Asn Met Val Arg Ser Gly Gln Val
115       120       125
Thr Ser Glu Glu Leu Val Asn Met Ala Tyr Asp Ile Ile Ala Lys Glu
130       135       140
Asn Pro Ser Leu Asn Ala Val Ile Thr Thr Arg Gln Glu Ala Ile
145       150       155       160
Glu Glu Ala Arg Lys Leu Lys Asp Thr Asn Gln Pro Phe Leu Gly Val
165       170       175
Pro Leu Leu Val Lys Gly Leu Gly His Ser Ile Lys Gly Gly Glu Thr
180       185       190
Asn Asn Gly Leu Ile Tyr Ala Asp Gly Lys Ile Ser Thr Phe Asp Ser
195       200       205
Ser Tyr Val Lys Lys Tyr Lys Asp Leu Gly Phe Ile Ile Leu Gly Gln
210       215       220
Thr Asn Phe Pro Glu Tyr Gly Trp Arg Asn Ile Thr Asp Ser Lys Leu
225       230       235       240
Tyr Gly Leu Thr His Asn Pro Trp Asp Leu Ala His Asn Ala Gly Gly
245       250       255
Ser Ser Gly Gly Ser Ala Ala Ala Ile Ala Ser Gly Met Thr Pro Ile
260       265       270
Ala Ser Gly Ser Asp Ala Gly Gly Ser Ile Arg Ile Pro Ser Ser Trp
275       280       285
Thr Gly Leu Val Gly Leu Lys Pro Thr Arg Gly Leu Val Ser Asn Glu
290       295       300
Lys Pro Asp Ser Tyr Ser Thr Ala Val His Phe Pro Leu Thr Lys Ser
305       310       315       320
Ser Arg Asp Ala Glu Thr Leu Leu Thr Tyr Leu Lys Lys Ser Asp Gln
325       330       335
Thr Leu Val Ser Val Asn Asp Leu Lys Ser Leu Pro Ile Ala Tyr Thr
340       345       350
Leu Lys Ser Pro Met Gly Thr Glu Val Ser Gln Asp Ala Lys Asn Ala
355       360       365

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Ile Met Asp Asn Val Thr Phe Leu Arg Lys Gln Gly Phe Lys Val Thr
  370                      375                      380

Glu Ile Asp Leu Pro Ile Asp Gly Arg Ala Leu Met Arg Asp Tyr Ser
  385                      390                      395                      400

Thr Leu Ala Ile Gly Met Gly Gly Ala Phe Ser Thr Ile Glu Lys Asp
                      405                      410                      415

Leu Lys Lys His Gly Phe Thr Lys Glu Asp Val Asp Pro Ile Thr Trp
                      420                      425                      430

Ala Val His Val Ile Tyr Gln Asn Ser Asp Lys Ala Glu Leu Lys Lys
                      435                      440                      445

Ser Ile Met Glu Ala Gln Lys His Met Asp Asp Tyr Arg Lys Ala Met
                      450                      455                      460

Glu Lys Leu His Lys Gln Phe Pro Ile Phe Leu Ser Pro Thr Thr Ala
  465                      470                      475                      480

Ser Leu Ala Pro Leu Asn Thr Asp Pro Tyr Val Thr Glu Glu Asp Lys
                      485                      490                      495

Arg Ala Ile Tyr Asn Met Glu Asn Leu Ser Gln Glu Glu Arg Ile Ala
                      500                      505                      510

Leu Phe Asn Arg Gln Trp Glu Pro Met Leu Arg Arg Thr Pro Phe Thr
                      515                      520                      525

Gln Ile Ala Asn Met Thr Gly Leu Pro Ala Ile Ser Ile Pro Thr Tyr
                      530                      535                      540

Leu Ser Glu Ser Gly Leu Pro Ile Gly Thr Met Leu Met Ala Gly Ala
  545                      550                      555                      560

Asn Tyr Asp Met Val Leu Ile Lys Phe Ala Thr Phe Phe Glu Lys His
                      565                      570                      575

His Gly Phe Asn Val Lys Trp Gln Arg Ile Ile Asp Lys Glu Val Lys
                      580                      585                      590

Pro Ser Thr Gly Leu Ile Gln Pro Thr Asn Ser Leu Phe Lys Ala His
                      595                      600                      605

Ser Ser Leu Val Asn Leu Glu Glu Asn Ser Gln Val Thr Gln Val Ser
                      610                      615                      620

Ile Ser Lys Lys Trp Met Lys Ser Ser Val Lys Asn Lys
  625                      630                      635

```

<210> SEQ ID NO 77

<211> LENGTH: 599

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 77

```

Thr Thr Asn Thr Ile Val Gln Thr Asn Asp Ser Asn Pro Thr Ala Lys
  1                      5                      10                      15

Phe Val Ser Glu Ser Gly Gln Ser Val Ile Gly Gln Val Lys Pro Asp
  20                      25                      30

Asn Ser Ala Ala Leu Thr Thr Val Asp Thr Pro His His Ile Ser Ala
  35                      40                      45

Pro Asp Ala Leu Lys Thr Thr Gln Ser Ser Pro Val Val Glu Ser Thr
  50                      55                      60

Ser Thr Lys Leu Thr Glu Glu Thr Tyr Lys Gln Lys Asp Gly Gln Asp
  65                      70                      75                      80

Leu Ala Asn Met Val Arg Ser Gly Gln Val Thr Ser Glu Glu Leu Val
  85                      90                      95

Asn Met Ala Tyr Asp Ile Ile Ala Lys Glu Asn Pro Ser Leu Asn Ala

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100							105					110				
Val	Ile	Thr	Thr	Arg	Arg	Gln	Glu	Ala	Ile	Glu	Glu	Ala	Arg	Lys	Leu	
		115					120					125				
Lys	Asp	Thr	Asn	Gln	Pro	Phe	Leu	Gly	Val	Pro	Leu	Leu	Val	Lys	Gly	
	130					135					140					
Leu	Gly	His	Ser	Ile	Lys	Gly	Gly	Glu	Thr	Asn	Asn	Gly	Leu	Ile	Tyr	
145					150					155					160	
Ala	Asp	Gly	Lys	Ile	Ser	Thr	Phe	Asp	Ser	Ser	Tyr	Val	Lys	Lys	Tyr	
				165					170					175		
Lys	Asp	Leu	Gly	Phe	Ile	Ile	Leu	Gly	Gln	Thr	Asn	Phe	Pro	Glu	Tyr	
		180						185					190			
Gly	Trp	Arg	Asn	Ile	Thr	Asp	Ser	Lys	Leu	Tyr	Gly	Leu	Thr	His	Asn	
	195						200					205				
Pro	Trp	Asp	Leu	Ala	His	Asn	Ala	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ala	
	210					215						220				
Ala	Ala	Ile	Ala	Ser	Gly	Met	Thr	Pro	Ile	Ala	Ser	Gly	Ser	Asp	Ala	
225					230					235					240	
Gly	Gly	Ser	Ile	Arg	Ile	Pro	Ser	Ser	Trp	Thr	Gly	Leu	Val	Gly	Leu	
				245					250					255		
Lys	Pro	Thr	Arg	Gly	Leu	Val	Ser	Asn	Glu	Lys	Pro	Asp	Ser	Tyr	Ser	
		260						265					270			
Thr	Ala	Val	His	Phe	Pro	Leu	Thr	Lys	Ser	Ser	Arg	Asp	Ala	Glu	Thr	
	275						280					285				
Leu	Leu	Thr	Tyr	Leu	Lys	Lys	Ser	Asp	Gln	Thr	Leu	Val	Ser	Val	Asn	
	290					295					300					
Asp	Leu	Lys	Ser	Leu	Pro	Ile	Ala	Tyr	Thr	Leu	Lys	Ser	Pro	Met	Gly	
305					310					315					320	
Thr	Glu	Val	Ser	Gln	Asp	Ala	Lys	Asn	Ala	Ile	Met	Asp	Asn	Val	Thr	
				325					330					335		
Phe	Leu	Arg	Lys	Gln	Gly	Phe	Lys	Val	Thr	Glu	Ile	Asp	Leu	Pro	Ile	
		340					345						350			
Asp	Gly	Arg	Ala	Leu	Met	Arg	Asp	Tyr	Ser	Thr	Leu	Ala	Ile	Gly	Met	
	355						360					365				
Gly	Gly	Ala	Phe	Ser	Thr	Ile	Glu	Lys	Asp	Leu	Lys	Lys	His	Gly	Phe	
	370					375					380					
Thr	Lys	Glu	Asp	Val	Asp	Pro	Ile	Thr	Trp	Ala	Val	His	Val	Ile	Tyr	
385					390					395					400	
Gln	Asn	Ser	Asp	Lys	Ala	Glu	Leu	Lys	Lys	Ser	Ile	Met	Glu	Ala	Gln	
			405						410					415		
Lys	His	Met	Asp	Asp	Tyr	Arg	Lys	Ala	Met	Glu	Lys	Leu	His	Lys	Gln	
		420						425					430			
Phe	Pro	Ile	Phe	Leu	Ser	Pro	Thr	Thr	Ala	Ser	Leu	Ala	Pro	Leu	Asn	
	435						440					445				
Thr	Asp	Pro	Tyr	Val	Thr	Glu	Glu	Asp	Lys	Arg	Ala	Ile	Tyr	Asn	Met	
	450					455					460					
Glu	Asn	Leu	Ser	Gln	Glu	Glu	Arg	Ile	Ala	Leu	Phe	Asn	Arg	Gln	Trp	
465					470					475					480	
Glu	Pro	Met	Leu	Arg	Arg	Thr	Pro	Phe	Thr	Gln	Ile	Ala	Asn	Met	Thr	
			485						490					495		
Gly	Leu	Pro	Ala	Ile	Ser	Ile	Pro	Thr	Tyr	Leu	Ser	Glu	Ser	Gly	Leu	
		500						505					510			
Pro	Ile	Gly	Thr	Met	Leu	Met	Ala	Gly	Ala	Asn	Tyr	Asp	Met	Val	Leu	
	515						520					525				

-continued

Ile Lys Phe Ala Thr Phe Phe Glu Lys His His Gly Phe Asn Val Lys
530 535 540

Trp Gln Arg Ile Ile Asp Lys Glu Val Lys Pro Ser Thr Gly Leu Ile
545 550 555 560

Gln Pro Thr Asn Ser Leu Phe Lys Ala His Ser Ser Leu Val Asn Leu
565 570 575

Glu Glu Asn Ser Gln Val Thr Gln Val Ser Ile Ser Lys Lys Trp Met
580 585 590

Lys Ser Ser Val Lys Asn Lys
595

<210> SEQ ID NO 78

<211> LENGTH: 1020

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 78

```
atgaaacgta ttgctgtttt aactagtggg ggtgacgccc ctggtatgaa cgctgctatc    60
cgtgcagttg ttcgtaaagc aatttctgaa ggtatggaag tttacggcat caaccaaggt    120
tactatggta tggtagacag ggataatttc cctttggatg ctaattctgt tggggatact    180
atcaaccgtg gaggaacggt tttacgttca gcacgttata ctgaatttgc tgaacttgaa    240
ggtcagctta aagggattga acagcttaaa aaacacggta ttgaagggtg agtagttatc    300
gggtggtgat gttcttatca tgggtgctatg cgtctaactg agcacggttt ccagctggtt    360
ggtttgccgg gtacaattga taacgataac gttggcactg actatactat tggttttgac    420
acagcagttg cgacagcagt tgagaatctt gaccgtcttc gtgatacatc agcaagtcac    480
aaccgtactt ttgttttgga gggttatgga agaaatgcag gagatatcgc tctttgggtca    540
ggtatcgctg cagggtgcaga tcaaattatt gttcctgaag aagagttcaa tattgatgaa    600
gttgtctcaa atgttagagc tgggtatgca gctggtaaac atcaccaaat catcgctcct    660
gcagaagggt ttatgagtgg tgatgagttt gcaaaaacaa tgaaagcagc aggagacgat    720
agcgatcttc gtgtgacgaa ttaggacatc ctgctccgtg gtggtagtcc gacggctcgt    780
gatcgtgtct tagcatctcg tatgggagcg tacgctgttc aattgttgaa agaaggctcg    840
gggtggttag ccgttggtgt ccacaacgaa gaaatggttg aaagtccaat tttaggttta    900
gcagaagaag gtgctttggt cagcttgact gatgaaggaa aatcgttgt taataatccg    960
cataaagcgg accttcgctt ggcagcactt aatcgtgacc ttgccaacca aagtagtaaa   1020
```

<210> SEQ ID NO 79

<211> LENGTH: 340

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 79

Met Lys Arg Ile Ala Val Leu Thr Ser Gly Gly Asp Ala Pro Gly Met
1 5 10 15

Asn Ala Ala Ile Arg Ala Val Val Arg Lys Ala Ile Ser Glu Gly Met
20 25 30

Glu Val Tyr Gly Ile Asn Gln Gly Tyr Tyr Gly Met Val Thr Gly Asp
35 40 45

Ile Phe Pro Leu Asp Ala Asn Ser Val Gly Asp Thr Ile Asn Arg Gly
50 55 60

Gly Thr Phe Leu Arg Ser Ala Arg Tyr Pro Glu Phe Ala Glu Leu Glu

-continued

65	70	75	80
Gly Gln Leu Lys Gly Ile Glu Gln Leu Lys Lys His Gly Ile Glu Gly	85	90	95
Val Val Val Ile Gly Gly Asp Gly Ser Tyr His Gly Ala Met Arg Leu	100	105	110
Thr Glu His Gly Phe Pro Ala Val Gly Leu Pro Gly Thr Ile Asp Asn	115	120	125
Asp Ile Val Gly Thr Asp Tyr Thr Ile Gly Phe Asp Thr Ala Val Ala	130	135	140
Thr Ala Val Glu Asn Leu Asp Arg Leu Arg Asp Thr Ser Ala Ser His	145	150	155
Asn Arg Thr Phe Val Val Glu Val Met Gly Arg Asn Ala Gly Asp Ile	165	170	175
Ala Leu Trp Ser Gly Ile Ala Ala Gly Ala Asp Gln Ile Ile Val Pro	180	185	190
Glu Glu Glu Phe Asn Ile Asp Glu Val Val Ser Asn Val Arg Ala Gly	195	200	205
Tyr Ala Ala Gly Lys His His Gln Ile Ile Val Leu Ala Glu Gly Val	210	215	220
Met Ser Gly Asp Glu Phe Ala Lys Thr Met Lys Ala Ala Gly Asp Asp	225	230	235
Ser Asp Leu Arg Val Thr Asn Leu Gly His Leu Leu Arg Gly Gly Ser	245	250	255
Pro Thr Ala Arg Asp Arg Val Leu Ala Ser Arg Met Gly Ala Tyr Ala	260	265	270
Val Gln Leu Leu Lys Glu Gly Arg Gly Gly Leu Ala Val Gly Val His	275	280	285
Asn Glu Glu Met Val Glu Ser Pro Ile Leu Gly Leu Ala Glu Glu Gly	290	295	300
Ala Leu Phe Ser Leu Thr Asp Glu Gly Lys Ile Val Val Asn Asn Pro	305	310	315
His Lys Ala Asp Leu Arg Leu Ala Ala Leu Asn Arg Asp Leu Ala Asn	325	330	335
Gln Ser Ser Lys	340		

<210> SEQ ID NO 80

<211> LENGTH: 2070

<212> TYPE: DNA

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 80

atgaaaaaga aaattatttt gaaaagtagt gttcttggtt tagtcgctgg gacttctatt	60
atgttctcaa gcgtgttcgc ggaccaagtc ggtgtccaag ttataggcgt caatgacttt	120
catggtgcac ttgacaatac tggaacagca aatatgcctg atggaaaagt tgctaattgct	180
ggtactgctg ctcaattaga tgcttatatg gatgacgctc aaaaagattt caaacaaact	240
aacctaatg gtgaaagcat tagggttcaa gcaggcgata tggttggagc aagtcagcc	300
aactctgggc ttcttcaaga tgaaccaact gtcaaaaatt ttaatgcaat gaatgttgag	360
tatggcacat tgggtaacca tgaatttgat gaagggttg cagaatataa tcgtatcgtt	420
actggtaaaag cccctgctcc agattcctaat attaataata ttacgaaatc ataccacat	480
gaagctgcaa aacaagaaat tgtagtgga aatgttattg ataaagttaa caaacaaatt	540

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ccttacaatt ggaagcctta cgctattaaa aatattcctg taaataacaa aagtgtgaac 600
gttggtcttta tcgggattgt caccaaagac atcccaaacc ttgtottacg taaaaattat 660
gaacaatatg aattttttaga tgaagctgaa acaatcgta aatacgccaa agaattacaa 720
gctaaaaatg tcaaagctat tgtagttctc gcacatgtac ctgcaacaag taaaaatgat 780
attgtctgaag gtgaagcagc agaaatgatg aaaaaagtca atcaactctt ccctgaaaat 840
agcgtagata ttgtctttgc tggacacaat catcaatata caaatggtct ttgttggtaaa 900
actcgtattg tacaagcgct ctctcaagga aaagcctatg ctgatgtacg tgggtgtctta 960
gatactgata cacaagattt cattgagacc ccttcagcta aagtaattgc agttgctcct 1020
ggtaaaaaaa caggtagtgc cgatattcaa gccattgttg accaagctaa tactatcggt 1080
aaacaagtaa cagaagctaa aattggtact gccgaggtaa gtgtcatgat tacgcgttct 1140
gttgatcaag ataattgttag tccggtaggc agcctcatca cagaggctca actagcaatt 1200
gctcgaaaaa gctggccaga tatcgatttt gccatgacaa ataatggtgg cattcgtgct 1260
gacttactca tcaaaccaga tggaacaatc acctggggag ctgcacaagc agttcaacct 1320
tttggttaata tcttacaagt cgtcgaaaat actggtagag atctttataa agcactcaac 1380
gaacaatacg accaaaaaca aaatttcttc cttcaaatag ctggtctgcg atacacttac 1440
acagataata aagagggcgg ggaagaaaca ccatttaaag ttgtaaaagc ttataaatca 1500
aatggtgagg aaatcaatcc tgatgcaaaa tacaatttag ttatcaatga ctttttattc 1560
gggtggtggt atggctttgc aagcttcaga aatgccaaac ttctaggagc cattaacccc 1620
gatacagagg tatttatggc ctatatcact gatttagaaa aagctggtaa aaaagtgagc 1680
gttccaaata ataaacctaa aatctatgtc actatgaaga tggttaatga aactattaca 1740
caaaatgatg gtacacatag cattattaag aaactttatt tagatcgaca aggaaatatt 1800
gtagcacaag agattgtatc agacacttta aaccaaaca aatcaaaatc taaaaaatc 1860
aaccctgtaa ctacaattca caaaaaaca ttacaccaat ttacagctat taaccctatg 1920
agaaattatg gcaaaccatc aaactccact actgtaaaat caaaacaatt accaaaaaca 1980
aactctgaat atggacaatc attccttatg tctgtctttg gtgttggtact tataggaatt 2040
gctttaataa caaagaaaaa acatatgaaa 2070

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<210> SEQ ID NO 81

<211> LENGTH: 690

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 81

```

Met Lys Lys Lys Ile Ile Leu Lys Ser Ser Val Leu Gly Leu Val Ala
  1             5             10             15

```

```

Gly Thr Ser Ile Met Phe Ser Ser Val Phe Ala Asp Gln Val Gly Val
      20             25             30

```

```

Gln Val Ile Gly Val Asn Asp Phe His Gly Ala Leu Asp Asn Thr Gly
    35             40             45

```

```

Thr Ala Asn Met Pro Asp Gly Lys Val Ala Asn Ala Gly Thr Ala Ala
    50             55             60

```

```

Gln Leu Asp Ala Tyr Met Asp Asp Ala Gln Lys Asp Phe Lys Gln Thr
    65             70             75             80

```

```

Asn Pro Asn Gly Glu Ser Ile Arg Val Gln Ala Gly Asp Met Val Gly
      85             90             95

```

```

Ala Ser Pro Ala Asn Ser Gly Leu Leu Gln Asp Glu Pro Thr Val Lys

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100						105						110			
Asn	Phe	Asn	Ala	Met	Asn	Val	Glu	Tyr	Gly	Thr	Leu	Gly	Asn	His	Glu
		115					120					125			
Phe	Asp	Glu	Gly	Leu	Ala	Glu	Tyr	Asn	Arg	Ile	Val	Thr	Gly	Lys	Ala
	130					135					140				
Pro	Ala	Pro	Asp	Ser	Asn	Ile	Asn	Asn	Ile	Thr	Lys	Ser	Tyr	Pro	His
145					150					155					160
Glu	Ala	Ala	Lys	Gln	Glu	Ile	Val	Val	Ala	Asn	Val	Ile	Asp	Lys	Val
			165						170					175	
Asn	Lys	Gln	Ile	Pro	Tyr	Asn	Trp	Lys	Pro	Tyr	Ala	Ile	Lys	Asn	Ile
		180						185					190		
Pro	Val	Asn	Asn	Lys	Ser	Val	Asn	Val	Gly	Phe	Ile	Gly	Ile	Val	Thr
	195						200					205			
Lys	Asp	Ile	Pro	Asn	Leu	Val	Leu	Arg	Lys	Asn	Tyr	Glu	Gln	Tyr	Glu
	210					215					220				
Phe	Leu	Asp	Glu	Ala	Glu	Thr	Ile	Val	Lys	Tyr	Ala	Lys	Glu	Leu	Gln
225					230					235					240
Ala	Lys	Asn	Val	Lys	Ala	Ile	Val	Val	Leu	Ala	His	Val	Pro	Ala	Thr
			245						250					255	
Ser	Lys	Asn	Asp	Ile	Ala	Glu	Gly	Glu	Ala	Ala	Glu	Met	Met	Lys	Lys
		260						265				270			
Val	Asn	Gln	Leu	Phe	Pro	Glu	Asn	Ser	Val	Asp	Ile	Val	Phe	Ala	Gly
	275						280					285			
His	Asn	His	Gln	Tyr	Thr	Asn	Gly	Leu	Val	Gly	Lys	Thr	Arg	Ile	Val
	290					295					300				
Gln	Ala	Leu	Ser	Gln	Gly	Lys	Ala	Tyr	Ala	Asp	Val	Arg	Gly	Val	Leu
305					310					315					320
Asp	Thr	Asp	Thr	Gln	Asp	Phe	Ile	Glu	Thr	Pro	Ser	Ala	Lys	Val	Ile
			325						330					335	
Ala	Val	Ala	Pro	Gly	Lys	Lys	Thr	Gly	Ser	Ala	Asp	Ile	Gln	Ala	Ile
		340						345					350		
Val	Asp	Gln	Ala	Asn	Thr	Ile	Val	Lys	Gln	Val	Thr	Glu	Ala	Lys	Ile
	355						360					365			
Gly	Thr	Ala	Glu	Val	Ser	Val	Met	Ile	Thr	Arg	Ser	Val	Asp	Gln	Asp
	370					375					380				
Asn	Val	Ser	Pro	Val	Gly	Ser	Leu	Ile	Thr	Glu	Ala	Gln	Leu	Ala	Ile
385					390					395					400
Ala	Arg	Lys	Ser	Trp	Pro	Asp	Ile	Asp	Phe	Ala	Met	Thr	Asn	Asn	Gly
			405						410					415	
Gly	Ile	Arg	Ala	Asp	Leu	Leu	Ile	Lys	Pro	Asp	Gly	Thr	Ile	Thr	Trp
		420						425					430		
Gly	Ala	Ala	Gln	Ala	Val	Gln	Pro	Phe	Gly	Asn	Ile	Leu	Gln	Val	Val
	435					440						445			
Glu	Ile	Thr	Gly	Arg	Asp	Leu	Tyr	Lys	Ala	Leu	Asn	Glu	Gln	Tyr	Asp
	450					455					460				
Gln	Lys	Gln	Asn	Phe	Phe	Leu	Gln	Ile	Ala	Gly	Leu	Arg	Tyr	Thr	Tyr
465					470					475					480
Thr	Asp	Asn	Lys	Glu	Gly	Gly	Glu	Glu	Thr	Pro	Phe	Lys	Val	Val	Lys
			485						490					495	
Ala	Tyr	Lys	Ser	Asn	Gly	Glu	Glu	Ile	Asn	Pro	Asp	Ala	Lys	Tyr	Lys
			500						505				510		
Leu	Val	Ile	Asn	Asp	Phe	Leu	Phe	Gly	Gly	Gly	Asp	Gly	Phe	Ala	Ser
		515					520					525			

-continued

Phe Arg Asn Ala Lys Leu Leu Gly Ala Ile Asn Pro Asp Thr Glu Val
 530 535 540
 Phe Met Ala Tyr Ile Thr Asp Leu Glu Lys Ala Gly Lys Lys Val Ser
 545 550 555 560
 Val Pro Asn Asn Lys Pro Lys Ile Tyr Val Thr Met Lys Met Val Asn
 565 570 575
 Glu Thr Ile Thr Gln Asn Asp Gly Thr His Ser Ile Ile Lys Lys Leu
 580 585 590
 Tyr Leu Asp Arg Gln Gly Asn Ile Val Ala Gln Glu Ile Val Ser Asp
 595 600 605
 Thr Leu Asn Gln Thr Lys Ser Lys Ser Thr Lys Ile Asn Pro Val Thr
 610 615 620
 Thr Ile His Lys Lys Gln Leu His Gln Phe Thr Ala Ile Asn Pro Met
 625 630 635 640
 Arg Asn Tyr Gly Lys Pro Ser Asn Ser Thr Thr Val Lys Ser Lys Gln
 645 650 655
 Leu Pro Lys Thr Asn Ser Glu Tyr Gly Gln Ser Phe Leu Met Ser Val
 660 665 670
 Phe Gly Val Gly Leu Ile Gly Ile Ala Leu Asn Thr Lys Lys Lys His
 675 680 685
 Met Lys
 690

<210> SEQ ID NO 82

<211> LENGTH: 650

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 82

His Gly Ala Leu Asp Asn Thr Gly Thr Ala Asn Met Pro Asp Gly Lys
 1 5 10 15
 Val Ala Asn Ala Gly Thr Ala Ala Gln Leu Asp Ala Tyr Met Asp Asp
 20 25 30
 Ala Gln Lys Asp Phe Lys Gln Thr Asn Pro Asn Gly Glu Ser Ile Arg
 35 40 45
 Val Gln Ala Gly Asp Met Val Gly Ala Ser Pro Ala Asn Ser Gly Leu
 50 55 60
 Leu Gln Asp Glu Pro Thr Val Lys Asn Phe Asn Ala Met Asn Val Glu
 65 70 75 80
 Tyr Gly Thr Leu Gly Asn His Glu Phe Asp Glu Gly Leu Ala Glu Tyr
 85 90 95
 Asn Arg Ile Val Thr Gly Lys Ala Pro Ala Pro Asp Ser Asn Ile Asn
 100 105 110
 Asn Ile Thr Lys Ser Tyr Pro His Glu Ala Ala Lys Gln Glu Ile Val
 115 120 125
 Val Ala Asn Val Ile Asp Lys Val Asn Lys Gln Ile Pro Tyr Asn Trp
 130 135 140
 Lys Pro Tyr Ala Ile Lys Asn Ile Pro Val Asn Asn Lys Ser Val Asn
 145 150 155 160
 Val Gly Phe Ile Gly Ile Val Thr Lys Asp Ile Pro Asn Leu Val Leu
 165 170 175
 Arg Lys Asn Tyr Glu Gln Tyr Glu Phe Leu Asp Glu Ala Glu Thr Ile
 180 185 190
 Val Lys Tyr Ala Lys Glu Leu Gln Ala Lys Asn Val Lys Ala Ile Val

-continued

195					200					205					
Val	Leu	Ala	His	Val	Pro	Ala	Thr	Ser	Lys	Asn	Asp	Ile	Ala	Glu	Gly
210						215					220				
Glu	Ala	Ala	Glu	Met	Met	Lys	Lys	Val	Asn	Gln	Leu	Phe	Pro	Glu	Asn
225					230					235					240
Ser	Val	Asp	Ile	Val	Phe	Ala	Gly	His	Asn	His	Gln	Tyr	Thr	Asn	Gly
				245					250					255	
Leu	Val	Gly	Lys	Thr	Arg	Ile	Val	Gln	Ala	Leu	Ser	Gln	Gly	Lys	Ala
			260					265					270		
Tyr	Ala	Asp	Val	Arg	Gly	Val	Leu	Asp	Thr	Asp	Thr	Gln	Asp	Phe	Ile
	275						280					285			
Glu	Thr	Pro	Ser	Ala	Lys	Val	Ile	Ala	Val	Ala	Pro	Gly	Lys	Lys	Thr
	290					295					300				
Gly	Ser	Ala	Asp	Ile	Gln	Ala	Ile	Val	Asp	Gln	Ala	Asn	Thr	Ile	Val
305					310					315					320
Lys	Gln	Val	Thr	Glu	Ala	Lys	Ile	Gly	Thr	Ala	Glu	Val	Ser	Val	Met
				325					330					335	
Ile	Thr	Arg	Ser	Val	Asp	Gln	Asp	Asn	Val	Ser	Pro	Val	Gly	Ser	Leu
			340					345					350		
Ile	Thr	Glu	Ala	Gln	Leu	Ala	Ile	Ala	Arg	Lys	Ser	Trp	Pro	Asp	Ile
	355					360						365			
Asp	Phe	Ala	Met	Thr	Asn	Asn	Gly	Gly	Ile	Arg	Ala	Asp	Leu	Leu	Ile
	370					375					380				
Lys	Pro	Asp	Gly	Thr	Ile	Thr	Trp	Gly	Ala	Ala	Gln	Ala	Val	Gln	Pro
385					390					395					400
Phe	Gly	Asn	Ile	Leu	Gln	Val	Val	Glu	Ile	Thr	Gly	Arg	Asp	Leu	Tyr
				405					410					415	
Lys	Ala	Leu	Asn	Glu	Gln	Tyr	Asp	Gln	Lys	Gln	Asn	Phe	Phe	Leu	Gln
			420					425					430		
Ile	Ala	Gly	Leu	Arg	Tyr	Thr	Tyr	Thr	Asp	Asn	Lys	Glu	Gly	Gly	Glu
	435					440						445			
Glu	Thr	Pro	Phe	Lys	Val	Val	Lys	Ala	Tyr	Lys	Ser	Asn	Gly	Glu	Glu
	450					455					460				
Ile	Asn	Pro	Asp	Ala	Lys	Tyr	Lys	Leu	Val	Ile	Asn	Asp	Phe	Leu	Phe
465					470					475					480
Gly	Gly	Gly	Asp	Gly	Phe	Ala	Ser	Phe	Arg	Asn	Ala	Lys	Leu	Leu	Gly
				485					490					495	
Ala	Ile	Asn	Pro	Asp	Thr	Glu	Val	Phe	Met	Ala	Tyr	Ile	Thr	Asp	Leu
			500					505					510		
Glu	Lys	Ala	Gly	Lys	Lys	Val	Ser	Val	Pro	Asn	Asn	Lys	Pro	Lys	Ile
	515					520						525			
Tyr	Val	Thr	Met	Lys	Met	Val	Asn	Glu	Thr	Ile	Thr	Gln	Asn	Asp	Gly
	530					535						540			
Thr	His	Ser	Ile	Ile	Lys	Lys	Leu	Tyr	Leu	Asp	Arg	Gln	Gly	Asn	Ile
545					550					555					560
Val	Ala	Gln	Glu	Ile	Val	Ser	Asp	Thr	Leu	Asn	Gln	Thr	Lys	Ser	Lys
				565					570					575	
Ser	Thr	Lys	Ile	Asn	Pro	Val	Thr	Thr	Ile	His	Lys	Lys	Gln	Leu	His
			580					585					590		
Gln	Phe	Thr	Ala	Ile	Asn	Pro	Met	Arg	Asn	Tyr	Gly	Lys	Pro	Ser	Asn
	595						600					605			
Ser	Thr	Thr	Val	Lys	Ser	Lys	Gln	Leu	Pro	Lys	Thr	Asn	Ser	Glu	Tyr
	610					615					620				

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Gly Gln Ser Phe Leu Met Ser Val Phe Gly Val Gly Leu Ile Gly Ile
625 630 635 640

Ala Leu Asn Thr Lys Lys Lys His Met Lys
645 650

<210> SEQ ID NO 83

<211> LENGTH: 654

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 83

Met Lys Lys Lys Ile Ile Leu Lys Ser Ser Val Leu Gly Leu Val Ala
1 5 10 15

Gly Thr Ser Ile Met Phe Ser Ser Val Phe Ala Asp Gln Val Gly Val
20 25 30

Gln Val Ile Gly Val Asn Asp Phe His Gly Ala Leu Asp Asn Thr Gly
35 40 45

Thr Ala Asn Met Pro Asp Gly Lys Val Ala Asn Ala Gly Thr Ala Ala
50 55 60

Gln Leu Asp Ala Tyr Met Asp Asp Ala Gln Lys Asp Phe Lys Gln Thr
65 70 75 80

Asn Pro Asn Gly Glu Ser Ile Arg Val Gln Ala Gly Asp Met Val Gly
85 90 95

Ala Ser Pro Ala Asn Ser Gly Leu Leu Gln Asp Glu Pro Thr Val Lys
100 105 110

Asn Phe Asn Ala Met Asn Val Glu Tyr Gly Thr Leu Gly Asn His Glu
115 120 125

Phe Asp Glu Gly Leu Ala Glu Tyr Asn Arg Ile Val Thr Gly Lys Ala
130 135 140

Pro Ala Pro Asp Ser Asn Ile Asn Asn Ile Thr Lys Ser Tyr Pro His
145 150 155 160

Glu Ala Ala Lys Gln Glu Ile Val Val Ala Asn Val Ile Asp Lys Val
165 170 175

Asn Lys Gln Ile Pro Tyr Asn Trp Lys Pro Tyr Ala Ile Lys Asn Ile
180 185 190

Pro Val Asn Asn Lys Ser Val Asn Val Gly Phe Ile Gly Ile Val Thr
195 200 205

Lys Asp Ile Pro Asn Leu Val Leu Arg Lys Asn Tyr Glu Gln Tyr Glu
210 215 220

Phe Leu Asp Glu Ala Glu Thr Ile Val Lys Tyr Ala Lys Glu Leu Gln
225 230 235 240

Ala Lys Asn Val Lys Ala Ile Val Val Leu Ala His Val Pro Ala Thr
245 250 255

Ser Lys Asn Asp Ile Ala Glu Gly Glu Ala Ala Glu Met Met Lys Lys
260 265 270

Val Asn Gln Leu Phe Pro Glu Asn Ser Val Asp Ile Val Phe Ala Gly
275 280 285

His Asn His Gln Tyr Thr Asn Gly Leu Val Gly Lys Thr Arg Ile Val
290 295 300

Gln Ala Leu Ser Gln Gly Lys Ala Tyr Ala Asp Val Arg Gly Val Leu
305 310 315 320

Asp Thr Asp Thr Gln Asp Phe Ile Glu Thr Pro Ser Ala Lys Val Ile
325 330 335

Ala Val Ala Pro Gly Lys Lys Thr Gly Ser Ala Asp Ile Gln Ala Ile

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340					345					350					
Val	Asp	Gln	Ala	Asn	Thr	Ile	Val	Lys	Gln	Val	Thr	Glu	Ala	Lys	Ile
	355						360					365			
Gly	Thr	Ala	Glu	Val	Ser	Val	Met	Ile	Thr	Arg	Ser	Val	Asp	Gln	Asp
	370					375					380				
Asn	Val	Ser	Pro	Val	Gly	Ser	Leu	Ile	Thr	Glu	Ala	Gln	Leu	Ala	Ile
385					390					395					400
Ala	Arg	Lys	Ser	Trp	Pro	Asp	Ile	Asp	Phe	Ala	Met	Thr	Asn	Asn	Gly
			405						410						415
Gly	Ile	Arg	Ala	Asp	Leu	Leu	Ile	Lys	Pro	Asp	Gly	Thr	Ile	Thr	Trp
			420					425						430	
Gly	Ala	Ala	Gln	Ala	Val	Gln	Pro	Phe	Gly	Asn	Ile	Leu	Gln	Val	Val
			435				440					445			
Glu	Ile	Thr	Gly	Arg	Asp	Leu	Tyr	Lys	Ala	Leu	Asn	Glu	Gln	Tyr	Asp
	450					455					460				
Gln	Lys	Gln	Asn	Phe	Phe	Leu	Gln	Ile	Ala	Gly	Leu	Arg	Tyr	Thr	Tyr
465					470					475					480
Thr	Asp	Asn	Lys	Glu	Gly	Gly	Glu	Glu	Thr	Pro	Phe	Lys	Val	Val	Lys
				485					490						495
Ala	Tyr	Lys	Ser	Asn	Gly	Glu	Glu	Ile	Asn	Pro	Asp	Ala	Lys	Tyr	Lys
			500					505					510		
Leu	Val	Ile	Asn	Asp	Phe	Leu	Phe	Gly	Gly	Gly	Asp	Gly	Phe	Ala	Ser
		515					520					525			
Phe	Arg	Asn	Ala	Lys	Leu	Leu	Gly	Ala	Ile	Asn	Pro	Asp	Thr	Glu	Val
	530					535					540				
Phe	Met	Ala	Tyr	Ile	Thr	Asp	Leu	Glu	Lys	Ala	Gly	Lys	Lys	Val	Ser
545					550					555					560
Val	Pro	Asn	Asn	Lys	Pro	Lys	Ile	Tyr	Val	Thr	Met	Lys	Met	Val	Asn
				565					570						575
Glu	Thr	Ile	Thr	Gln	Asn	Asp	Gly	Thr	His	Ser	Ile	Ile	Lys	Lys	Leu
			580					585						590	
Tyr	Leu	Asp	Arg	Gln	Gly	Asn	Ile	Val	Ala	Gln	Glu	Ile	Val	Ser	Asp
	595					600						605			
Thr	Leu	Asn	Gln	Thr	Lys	Ser	Lys	Ser	Thr	Lys	Ile	Asn	Pro	Val	Thr
	610					615					620				
Thr	Ile	His	Lys	Lys	Gln	Leu	His	Gln	Phe	Thr	Ala	Ile	Asn	Pro	Met
625					630					635					640
Arg	Asn	Tyr	Gly	Lys	Pro	Ser	Asn	Ser	Thr	Val	Lys	Ser			
			645						650						

<210> SEQ ID NO 84

<211> LENGTH: 614

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 84

His	Gly	Ala	Leu	Asp	Asn	Thr	Gly	Thr	Ala	Asn	Met	Pro	Asp	Gly	Lys
1				5					10					15	
Val	Ala	Asn	Ala	Gly	Thr	Ala	Ala	Gln	Leu	Asp	Ala	Tyr	Met	Asp	Asp
			20					25					30		
Ala	Gln	Lys	Asp	Phe	Lys	Gln	Thr	Asn	Pro	Asn	Gly	Glu	Ser	Ile	Arg
		35					40					45			
Val	Gln	Ala	Gly	Asp	Met	Val	Gly	Ala	Ser	Pro	Ala	Asn	Ser	Gly	Leu
	50					55					60				

-continued

Leu	Gln	Asp	Glu	Pro	Thr	Val	Lys	Asn	Phe	Asn	Ala	Met	Asn	Val	Glu	65	70	75	80
Tyr	Gly	Thr	Leu	Gly	Asn	His	Glu	Phe	Asp	Glu	Gly	Leu	Ala	Glu	Tyr	85	90	95	
Asn	Arg	Ile	Val	Thr	Gly	Lys	Ala	Pro	Ala	Pro	Asp	Ser	Asn	Ile	Asn	100	105	110	
Asn	Ile	Thr	Lys	Ser	Tyr	Pro	His	Glu	Ala	Ala	Lys	Gln	Glu	Ile	Val	115	120	125	
Val	Ala	Asn	Val	Ile	Asp	Lys	Val	Asn	Lys	Gln	Ile	Pro	Tyr	Asn	Trp	130	135	140	
Lys	Pro	Tyr	Ala	Ile	Lys	Asn	Ile	Pro	Val	Asn	Asn	Lys	Ser	Val	Asn	145	150	155	160
Val	Gly	Phe	Ile	Gly	Ile	Val	Thr	Lys	Asp	Ile	Pro	Asn	Leu	Val	Leu	165	170	175	
Arg	Lys	Asn	Tyr	Glu	Gln	Tyr	Glu	Phe	Leu	Asp	Glu	Ala	Glu	Thr	Ile	180	185	190	
Val	Lys	Tyr	Ala	Lys	Glu	Leu	Gln	Ala	Lys	Asn	Val	Lys	Ala	Ile	Val	195	200	205	
Val	Leu	Ala	His	Val	Pro	Ala	Thr	Ser	Lys	Asn	Asp	Ile	Ala	Glu	Gly	210	215	220	
Glu	Ala	Ala	Glu	Met	Met	Lys	Lys	Val	Asn	Gln	Leu	Phe	Pro	Glu	Asn	225	230	235	240
Ser	Val	Asp	Ile	Val	Phe	Ala	Gly	His	Asn	His	Gln	Tyr	Thr	Asn	Gly	245	250	255	
Leu	Val	Gly	Lys	Thr	Arg	Ile	Val	Gln	Ala	Leu	Ser	Gln	Gly	Lys	Ala	260	265	270	
Tyr	Ala	Asp	Val	Arg	Gly	Val	Leu	Asp	Thr	Asp	Thr	Gln	Asp	Phe	Ile	275	280	285	
Glu	Thr	Pro	Ser	Ala	Lys	Val	Ile	Ala	Val	Ala	Pro	Gly	Lys	Lys	Thr	290	295	300	
Gly	Ser	Ala	Asp	Ile	Gln	Ala	Ile	Val	Asp	Gln	Ala	Asn	Thr	Ile	Val	305	310	315	320
Lys	Gln	Val	Thr	Glu	Ala	Lys	Ile	Gly	Thr	Ala	Glu	Val	Ser	Val	Met	325	330	335	
Ile	Thr	Arg	Ser	Val	Asp	Gln	Asp	Asn	Val	Ser	Pro	Val	Gly	Ser	Leu	340	345	350	
Ile	Thr	Glu	Ala	Gln	Leu	Ala	Ile	Ala	Arg	Lys	Ser	Trp	Pro	Asp	Ile	355	360	365	
Asp	Phe	Ala	Met	Thr	Asn	Asn	Gly	Gly	Ile	Arg	Ala	Asp	Leu	Leu	Ile	370	375	380	
Lys	Pro	Asp	Gly	Thr	Ile	Thr	Trp	Gly	Ala	Ala	Gln	Ala	Val	Gln	Pro	385	390	395	400
Phe	Gly	Asn	Ile	Leu	Gln	Val	Val	Glu	Ile	Thr	Gly	Arg	Asp	Leu	Tyr	405	410	415	
Lys	Ala	Leu	Asn	Glu	Gln	Tyr	Asp	Gln	Lys	Gln	Asn	Phe	Phe	Leu	Gln	420	425	430	
Ile	Ala	Gly	Leu	Arg	Tyr	Thr	Tyr	Thr	Asp	Asn	Lys	Glu	Gly	Gly	Glu	435	440	445	
Glu	Thr	Pro	Phe	Lys	Val	Val	Lys	Ala	Tyr	Lys	Ser	Asn	Gly	Glu	Glu	450	455	460	
Ile	Asn	Pro	Asp	Ala	Lys	Tyr	Lys	Leu	Val	Ile	Asn	Asp	Phe	Leu	Phe	465	470	475	480
Gly	Gly	Gly	Asp	Gly	Phe	Ala	Ser	Phe	Arg	Asn	Ala	Lys	Leu	Leu	Gly				

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485	490	495	
Ala Ile Asn Pro Asp Thr Glu Val Phe Met Ala Tyr Ile Thr Asp Leu			
500	505	510	
Glu Lys Ala Gly Lys Lys Val Ser Val Pro Asn Asn Lys Pro Lys Ile			
515	520	525	
Tyr Val Thr Met Lys Met Val Asn Glu Thr Ile Thr Gln Asn Asp Gly			
530	535	540	
Thr His Ser Ile Ile Lys Lys Leu Tyr Leu Asp Arg Gln Gly Asn Ile			
545	550	555	560
Val Ala Gln Glu Ile Val Ser Asp Thr Leu Asn Gln Thr Lys Ser Lys			
565	570	575	
Ser Thr Lys Ile Asn Pro Val Thr Thr Ile His Lys Lys Gln Leu His			
580	585	590	
Gln Phe Thr Ala Ile Asn Pro Met Arg Asn Tyr Gly Lys Pro Ser Asn			
595	600	605	
Ser Thr Thr Val Lys Ser			
610			
<210> SEQ ID NO 85			
<211> LENGTH: 783			
<212> TYPE: DNA			
<213> ORGANISM: Streptococcus agalactiae			
<400> SEQUENCE: 85			
atgaaaagat tacataaact gtttataacc gtaattgcta cattaggtat gttgggggta			60
atgacctttg gtcttccaac gcagccgcaa aacgtaacgc cgatagtaca tgctgatgtc			120
aattcatctg ttgatacgag ccaggaattt caaaataatt taaaaaatgc tattggtaac			180
ctaccatttc aatatgttaa tgggtattat gaattaaata ataatacagac aaatttaa			240
gctgatgtca atgttaaagc gtatgttcaa aatacaattg acaatcaaca aagactatca			300
actgctaatt caatgcttga tagaaccatt cgtcaatatc aaaatcgag agataccact			360
cttcccgatg caaattggaa accattaggt tggcatcaag tagctactaa tgaccattat			420
ggacatgcag tcgacaaggg gcatttaatt gcctatgctt tagctggaaa tttcaaaggt			480
tgggatgctt ccgtgtcaaa tcctcaaaat gttgtcacac aaacagctca ttccaaccaa			540
tcaaatcaaa aatatcaatcg tggacaaaat tattatgaaa gcttagttcg taaggcgggt			600
gacaaaaca aacgtgttcg ttaccgtgta actccattgt accgtaatga tactgattta			660
gttccatttg caatgcacct agaagctaaa tcacaagatg gcacattaga atttaattgt			720
gctattccaa acacacaagc atcatacact atggattatg caacaggaga aataacacta			780
aat			783

<210> SEQ ID NO 86
 <211> LENGTH: 261
 <212> TYPE: PRT
 <213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 86

Met Lys Arg Leu His Lys Leu Phe Ile Thr Val Ile Ala Thr Leu Gly			
1	5	10	15
Met Leu Gly Val Met Thr Phe Gly Leu Pro Thr Gln Pro Gln Asn Val			
20	25	30	
Thr Pro Ile Val His Ala Asp Val Asn Ser Ser Val Asp Thr Ser Gln			
35	40	45	

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Glu Phe Gln Asn Asn Leu Lys Asn Ala Ile Gly Asn Leu Pro Phe Gln
 50 55 60
 Tyr Val Asn Gly Ile Tyr Glu Leu Asn Asn Asn Gln Thr Asn Leu Asn
 65 70 75 80
 Ala Asp Val Asn Val Lys Ala Tyr Val Gln Asn Thr Ile Asp Asn Gln
 85 90 95
 Gln Arg Leu Ser Thr Ala Asn Ala Met Leu Asp Arg Thr Ile Arg Gln
 100 105 110
 Tyr Gln Asn Arg Arg Asp Thr Thr Leu Pro Asp Ala Asn Trp Lys Pro
 115 120 125
 Leu Gly Trp His Gln Val Ala Thr Asn Asp His Tyr Gly His Ala Val
 130 135 140
 Asp Lys Gly His Leu Ile Ala Tyr Ala Leu Ala Gly Asn Phe Lys Gly
 145 150 155 160
 Trp Asp Ala Ser Val Ser Asn Pro Gln Asn Val Val Thr Gln Thr Ala
 165 170 175
 His Ser Asn Gln Ser Asn Gln Lys Ile Asn Arg Gly Gln Asn Tyr Tyr
 180 185 190
 Glu Ser Leu Val Arg Lys Ala Val Asp Gln Asn Lys Arg Val Arg Tyr
 195 200 205
 Arg Val Thr Pro Leu Tyr Arg Asn Asp Thr Asp Leu Val Pro Phe Ala
 210 215 220
 Met His Leu Glu Ala Lys Ser Gln Asp Gly Thr Leu Glu Phe Asn Val
 225 230 235 240
 Ala Ile Pro Asn Thr Gln Ala Ser Tyr Thr Met Asp Tyr Ala Thr Gly
 245 250 255
 Glu Ile Thr Leu Asn
 260

<210> SEQ ID NO 87
 <211> LENGTH: 2703
 <212> TYPE: DNA
 <213> ORGANISM: Streptococcus agalactiae
 <400> SEQUENCE: 87

atgagaaaat accaaaaatt ttctaaaata ttgacgttaa gtcttttttg tttgtcgcaa	60
ataccgctta ataccaatgt tttaggggaa agtaccgtac cggaaaatgg tgctaaagga	120
aagttagttg ttaaaaagac agatgaccag aacaaaccac tttcaaaagc tacctttggt	180
ttaaaaacta ctgctcatcc agaaagtaaa atagaaaaag taactgctga gctaacagggt	240
gaagctactt ttgataatct catacctgga gattatactt tatcagaaga aacagcgccc	300
gaagggtata aaaagactaa ccagacttgg caagttaagg ttgagagtaa tggaaaaact	360
acgatacaaa atagtgggtga taaaaattcc acaattggac aaaatcagga agaactagat	420
aagcagtatc ccccccacagg aatttatgaa gatacaaaagg aatcttataa acttgagcat	480
gttaaagggt cagttccaaa tggaaagtca gaggcaaaag cagttaaccc atattcaagt	540
gaaggtgagc atataagaga aattccagag ggaacattat ctaaactgat ttcagaagta	600
gggtgatttag ctcataataa atataaaatt gagttaactg tcagtggaaa aaccatagta	660
aaaccagtgg acaaaacaaa gccgtagat gttgtcttcg tactcgataa ttctaactca	720
atgaataacg atggcccaaa ttttcaaagg cataataaag ccaagaaagc tgccgaagct	780
cttgggaccg cagtaaaaga tatttttagga gcaaacagtg ataatagggt tgcattagtt	840
acctatgggt catagatttt tgatggtagg agttagatg tcgtaaaagg atttaaagaa	900

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gatgataaat attatggcct tcaaactaag ttcacaattc agacagagaa ttatagtcac   960
aaacaattaa caaataatgc tgaagagatt ataaaaagga ttccgacaga agtcctataa  1020
gctaagtggg gatctactac caatggatta actccagagc aacaaaagga gtactatcct  1080
agtaaagtag gagaaacatt tactatgaaa gccttcattg aggagatga tattttgagt  1140
caagtaaadc gaaatagtca aaaaattatt gttcatgtaa ctgatggtgt tcctacgaga  1200
tcatatgcta ttaataattt taaactgggt gcatcatatg aaagccaatt tgaacaaatg  1260
aaaaaaaaat gatatctaaa taaaagtaat tttctactta ctgataagcc cgaggatata  1320
aaaggaaatg gggagagtta ctttttgttt cccttagata gttatcaaac acagataatc  1380
tctggaaact tacaaaaact tcattattta gatttaaadc ttaattaccc taaaggatca  1440
atztatcgaa atggaccagt gaaagaacat ggaacaccaa ccaaaactta tataaatagt  1500
ttaaacaga aaaattatga catttttaac tttggtatcg atatatctgg ttttagacaa  1560
gtttataatg aggagtataa gaaaaatcaa gatggtactt ttcaaaaatt gaaagaggaa  1620
gcttttaaac tttcagatgg agaaatcaca gaactaatga ggtcgttctc ttccaaacct  1680
gagtactaca cccctatcgt aacttcagcc gatacatcta acaatgaaat tttatctaaa  1740
attcagcaac aatttgaaac gattttaaca aaagaaaact caattgttaa tggaactatc  1800
gaagatccta tgggtgataa aatcaattta cagcttggtg atggacaaac attacagcca  1860
agtgattata ctttacaggg aaatgatgga agtgtaatga aggatggtat tgcaactggt  1920
gggcctaata atgatggtg aatacttaag ggggttaaat tagaatacat cggaaataaa  1980
ctctatgcta gaggtttgaa tttaggagaa ggtcaaaaag taacactcac atatgatgtg  2040
aaactagatg acagttttat aagtaacaaa ttctatgaca ctaatggtag aacaacattg  2100
aatcctaagt cagaggatcc taatacactt agagattttc caatccctaa aattcgtgat  2160
gtgagagaat atcctacaat aacgattaaa aacgagaaga agttaggtga aattgaattt  2220
ataaaagttg ataaagataa taataagttg cttctcaaag gagctacgtt tgaacttcaa  2280
gaatttaatg aagattataa actttattta ccaataaaaa ataataattc aaaagtagtg  2340
acgggagaaa acggcaaaat ttcttacaaa gatttgaaag atggcaaata tcagttaata  2400
gaagcagttt cgccggagga ttatcaaaaa attactaata aaccaatttt aacttttgaa  2460
gtggttaaag gatcgataaa aaatataata gctgttaata aacagatttc tgaatatcat  2520
gaggaagggtg acaagcattt aattaccaac acgcatattc caccaaaagg aattattcct  2580
atgacagggtg ggaaggaat tctatctttc attttaatag gtggagctat gatgtctatt  2640
gcagggtgaa tttatatattg gaaaagggtat aagaaatcta gtgatatgtc catcaaaaaa  2700
gat                                                                    2703

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<210> SEQ ID NO 88

<211> LENGTH: 901

<212> TYPE: PRT

<213> ORGANISM: Streptococcus agalactiae

<400> SEQUENCE: 88

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Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe
  1             5             10             15

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Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr
  20             25             30

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Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp
  35             40             45

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Asp 50	Gln	Asn	Lys	Pro	Leu	Ser 55	Lys	Ala	Thr	Phe	Val 60	Leu	Lys	Thr	Thr
Ala 65	His	Pro	Glu	Ser	Lys 70	Ile	Glu	Lys	Val	Thr 75	Ala	Glu	Leu	Thr	Gly 80
Glu	Ala	Thr	Phe	Asp 85	Asn	Leu	Ile	Pro	Gly 90	Asp	Tyr	Thr	Leu	Ser 95	Glu
Glu	Thr	Ala	Pro	Glu 100	Gly	Tyr	Lys	Lys 105	Thr	Asn	Gln	Thr	Trp 110	Gln	Val
Lys	Val	Glu	Ser	Asn 115	Gly	Lys	Thr	Thr 120	Ile	Gln	Asn	Ser 125	Gly	Asp	Lys
Asn	Ser	Thr	Ile	Gly 130	Gln	Asn	Gln	Glu 135	Glu	Leu	Asp 140	Lys	Gln	Tyr	Pro
Pro 145	Thr	Gly	Ile	Tyr	Glu 150	Asp	Thr	Lys	Glu	Ser 155	Tyr	Lys	Leu	Glu	His 160
Val	Lys	Gly	Ser	Val 165	Pro	Asn	Gly	Lys	Ser 170	Glu	Ala	Lys	Ala	Val 175	Asn
Pro	Tyr	Ser	Ser	Glu 180	Gly	Glu	His	Ile 185	Arg	Glu	Ile	Pro	Glu 190	Gly	Thr
Leu	Ser	Lys	Arg	Ile 195	Ser	Glu	Val	Gly 200	Asp	Leu	Ala	His 205	Asn	Lys	Tyr
Lys	Ile	Glu	Leu	Thr 210	Val	Ser	Gly	Lys 215	Thr	Ile	Val 220	Lys	Pro	Val	Asp
Lys 225	Gln	Lys	Pro	Leu	Asp 230	Val	Val	Phe	Val	Leu 235	Asp	Asn	Ser	Asn	Ser 240
Met	Asn	Asn	Asp	Gly 245	Pro	Asn	Phe	Gln	Arg 250	His	Asn	Lys	Ala	Lys 255	Lys
Ala	Ala	Glu	Ala	Leu 260	Gly	Thr	Ala	Val 265	Lys	Asp	Ile	Leu 270	Gly	Ala	Asn
Ser	Asp	Asn	Arg	Val 275	Ala	Leu	Val	Thr 280	Tyr	Gly	Ser	Asp 285	Ile	Phe	Asp
Gly	Arg	Ser	Val	Asp 290	Val	Val	Lys	Gly 295	Phe	Lys	Glu 300	Asp	Asp	Lys	Tyr
Tyr 305	Gly	Leu	Gln	Thr	Lys 310	Phe	Thr	Ile	Gln	Thr 315	Glu	Asn	Tyr	Ser	His 320
Lys	Gln	Leu	Thr	Asn 325	Asn	Ala	Glu	Glu	Ile 330	Ile	Lys	Arg	Ile	Pro 335	Thr
Glu	Ala	Pro	Lys	Ala 340	Lys	Trp	Gly	Ser 345	Thr	Thr	Asn	Gly	Leu 350	Thr	Pro
Glu	Gln	Gln	Lys	Glu 355	Tyr	Tyr	Leu	Ser 360	Lys	Val	Gly	Glu 365	Thr	Phe	Thr
Met 370	Lys	Ala	Phe	Met	Glu 375	Ala	Asp	Asp	Ile	Leu	Ser 380	Gln	Val	Asn	Arg
Asn 385	Ser	Gln	Lys	Ile	Ile 390	Val	His	Val	Thr	Asp 395	Gly	Val	Pro	Thr	Arg 400
Ser	Tyr	Ala	Ile	Asn 405	Asn	Phe	Lys	Leu	Gly 410	Ala	Ser	Tyr	Glu	Ser 415	Gln
Phe	Glu	Gln	Met	Lys 420	Lys	Asn	Gly	Tyr	Leu	Asn 425	Lys	Ser	Asn	Phe	Leu
Leu	Thr	Asp	Lys	Pro 435	Glu	Asp	Ile	Lys 440	Gly	Asn	Gly	Glu 445	Ser	Tyr	Phe
Leu 450	Phe	Pro	Leu	Asp	Ser 455	Tyr	Gln	Thr	Gln	Ile 460	Ile	Ser	Gly	Asn	Leu

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Gln	Lys	Leu	His	Tyr	Leu	Asp	Leu	Asn	Leu	Asn	Tyr	Pro	Lys	Gly	Thr	465	470	475	480
Ile	Tyr	Arg	Asn	Gly	Pro	Val	Lys	Glu	His	Gly	Thr	Pro	Thr	Lys	Leu	485	490	495	
Tyr	Ile	Asn	Ser	Leu	Lys	Gln	Lys	Asn	Tyr	Asp	Ile	Phe	Asn	Phe	Gly	500	505	510	
Ile	Asp	Ile	Ser	Gly	Phe	Arg	Gln	Val	Tyr	Asn	Glu	Glu	Tyr	Lys	Lys	515	520	525	
Asn	Gln	Asp	Gly	Thr	Phe	Gln	Lys	Leu	Lys	Glu	Glu	Ala	Phe	Lys	Leu	530	535	540	
Ser	Asp	Gly	Glu	Ile	Thr	Glu	Leu	Met	Arg	Ser	Phe	Ser	Ser	Lys	Pro	545	550	555	560
Glu	Tyr	Tyr	Thr	Pro	Ile	Val	Thr	Ser	Ala	Asp	Thr	Ser	Asn	Asn	Glu	565	570	575	
Ile	Leu	Ser	Lys	Ile	Gln	Gln	Gln	Phe	Glu	Thr	Ile	Leu	Thr	Lys	Glu	580	585	590	
Asn	Ser	Ile	Val	Asn	Gly	Thr	Ile	Glu	Asp	Pro	Met	Gly	Asp	Lys	Ile	595	600	605	
Asn	Leu	Gln	Leu	Gly	Asn	Gly	Gln	Thr	Leu	Gln	Pro	Ser	Asp	Tyr	Thr	610	615	620	
Leu	Gln	Gly	Asn	Asp	Gly	Ser	Val	Met	Lys	Asp	Gly	Ile	Ala	Thr	Gly	625	630	635	640
Gly	Pro	Asn	Asn	Asp	Gly	Gly	Ile	Leu	Lys	Gly	Val	Lys	Leu	Glu	Tyr	645	650	655	
Ile	Gly	Asn	Lys	Leu	Tyr	Val	Arg	Gly	Leu	Asn	Leu	Gly	Glu	Gly	Gln	660	665	670	
Lys	Val	Thr	Leu	Thr	Tyr	Asp	Val	Lys	Leu	Asp	Asp	Ser	Phe	Ile	Ser	675	680	685	
Asn	Lys	Phe	Tyr	Asp	Thr	Asn	Gly	Arg	Thr	Thr	Leu	Asn	Pro	Lys	Ser	690	695	700	
Glu	Asp	Pro	Asn	Thr	Leu	Arg	Asp	Phe	Pro	Ile	Pro	Lys	Ile	Arg	Asp	705	710	715	720
Val	Arg	Glu	Tyr	Pro	Thr	Ile	Thr	Ile	Lys	Asn	Glu	Lys	Lys	Leu	Gly	725	730	735	
Glu	Ile	Glu	Phe	Ile	Lys	Val	Asp	Lys	Asp	Asn	Asn	Lys	Leu	Leu	Leu	740	745	750	
Lys	Gly	Ala	Thr	Phe	Glu	Leu	Gln	Glu	Phe	Asn	Glu	Asp	Tyr	Lys	Leu	755	760	765	
Tyr	Leu	Pro	Ile	Lys	Asn	Asn	Asn	Ser	Lys	Val	Val	Thr	Gly	Glu	Asn	770	775	780	
Gly	Lys	Ile	Ser	Tyr	Lys	Asp	Leu	Lys	Asp	Gly	Lys	Tyr	Gln	Leu	Ile	785	790	795	800
Glu	Ala	Val	Ser	Pro	Glu	Asp	Tyr	Gln	Lys	Ile	Thr	Asn	Lys	Pro	Ile	805	810	815	
Leu	Thr	Phe	Glu	Val	Val	Lys	Gly	Ser	Ile	Lys	Asn	Ile	Ile	Ala	Val	820	825	830	
Asn	Lys	Gln	Ile	Ser	Glu	Tyr	His	Glu	Glu	Gly	Asp	Lys	His	Leu	Ile	835	840	845	
Thr	Asn	Thr	His	Ile	Pro	Pro	Lys	Gly	Ile	Ile	Pro	Met	Thr	Gly	Gly	850	855	860	
Lys	Gly	Ile	Leu	Ser	Phe	Ile	Leu	Ile	Gly	Gly	Ala	Met	Met	Ser	Ile	865	870	875	880
Ala	Gly	Gly	Ile	Tyr	Ile	Trp	Lys	Arg	Tyr	Lys	Lys	Ser	Ser	Asp	Met				

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885	890	895
Ser Ile Lys Lys Asp 900		
 <210> SEQ ID NO 89		
<211> LENGTH: 869		
<212> TYPE: PRT		
<213> ORGANISM: Streptococcus agalactiae		
 <400> SEQUENCE: 89		
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Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr 20 25 30		
Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp 35 40 45		
Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr 50 55 60		
Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly 65 70 75 80		
Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu 85 90 95		
Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val 100 105 110		
Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys 115 120 125		
Asn Ser Thr Ile Gly Gln Asn Gln Glu Glu Leu Asp Lys Gln Tyr Pro 130 135 140		
Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His 145 150 155 160		
Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn 165 170 175		
Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr 180 185 190		
Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr 195 200 205		
Lys Ile Glu Leu Thr Val Ser Gly Lys Thr Ile Val Lys Pro Val Asp 210 215 220		
Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser 225 230 235 240		
Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys 245 250 255		
Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn 260 265 270		
Ser Asp Asn Arg Val Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp 275 280 285		
Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr 290 295 300		
Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His 305 310 315 320		
Lys Gln Leu Thr Asn Asn Ala Glu Glu Ile Ile Lys Arg Ile Pro Thr 325 330 335		
Glu Ala Pro Lys Ala Lys Trp Gly Ser Thr Thr Asn Gly Leu Thr Pro 340 345 350		

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Glu	Gln	Gln	Lys	Glu	Tyr	Tyr	Leu	Ser	Lys	Val	Gly	Glu	Thr	Phe	Thr
		355					360					365			
Met	Lys	Ala	Phe	Met	Glu	Ala	Asp	Asp	Ile	Leu	Ser	Gln	Val	Asn	Arg
		370				375					380				
Asn	Ser	Gln	Lys	Ile	Ile	Val	His	Val	Thr	Asp	Gly	Val	Pro	Thr	Arg
385					390					395					400
Ser	Tyr	Ala	Ile	Asn	Asn	Phe	Lys	Leu	Gly	Ala	Ser	Tyr	Glu	Ser	Gln
				405					410					415	
Phe	Glu	Gln	Met	Lys	Lys	Asn	Gly	Tyr	Leu	Asn	Lys	Ser	Asn	Phe	Leu
			420					425					430		
Leu	Thr	Asp	Lys	Pro	Glu	Asp	Ile	Lys	Gly	Asn	Gly	Glu	Ser	Tyr	Phe
		435					440					445			
Leu	Phe	Pro	Leu	Asp	Ser	Tyr	Gln	Thr	Gln	Ile	Ile	Ser	Gly	Asn	Leu
		450				455					460				
Gln	Lys	Leu	His	Tyr	Leu	Asp	Leu	Asn	Leu	Asn	Tyr	Pro	Lys	Gly	Thr
465					470					475					480
Ile	Tyr	Arg	Asn	Gly	Pro	Val	Lys	Glu	His	Gly	Thr	Pro	Thr	Lys	Leu
			485						490					495	
Tyr	Ile	Asn	Ser	Leu	Lys	Gln	Lys	Asn	Tyr	Asp	Ile	Phe	Asn	Phe	Gly
			500					505				510			
Ile	Asp	Ile	Ser	Gly	Phe	Arg	Gln	Val	Tyr	Asn	Glu	Glu	Tyr	Lys	Lys
		515					520					525			
Asn	Gln	Asp	Gly	Thr	Phe	Gln	Lys	Leu	Lys	Glu	Glu	Ala	Phe	Lys	Leu
		530				535					540				
Ser	Asp	Gly	Glu	Ile	Thr	Glu	Leu	Met	Arg	Ser	Phe	Ser	Ser	Lys	Pro
545					550					555					560
Glu	Tyr	Tyr	Thr	Pro	Ile	Val	Thr	Ser	Ala	Asp	Thr	Ser	Asn	Asn	Glu
				565					570					575	
Ile	Leu	Ser	Lys	Ile	Gln	Gln	Gln	Phe	Glu	Thr	Ile	Leu	Thr	Lys	Glu
			580					585				590			
Asn	Ser	Ile	Val	Asn	Gly	Thr	Ile	Glu	Asp	Pro	Met	Gly	Asp	Lys	Ile
		595					600					605			
Asn	Leu	Gln	Leu	Gly	Asn	Gly	Gln	Thr	Leu	Gln	Pro	Ser	Asp	Tyr	Thr
		610			615						620				
Leu	Gln	Gly	Asn	Asp	Gly	Ser	Val	Met	Lys	Asp	Gly	Ile	Ala	Thr	Gly
		625			630					635					640
Gly	Pro	Asn	Asn	Asp	Gly	Gly	Ile	Leu	Lys	Gly	Val	Lys	Leu	Glu	Tyr
			645					650				655			
Ile	Gly	Asn	Lys	Leu	Tyr	Val	Arg	Gly	Leu	Asn	Leu	Gly	Glu	Gly	Gln
			660					665				670			
Lys	Val	Thr	Leu	Thr	Tyr	Asp	Val	Lys	Leu	Asp	Asp	Ser	Phe	Ile	Ser
		675					680					685			
Asn	Lys	Phe	Tyr	Asp	Thr	Asn	Gly	Arg	Thr	Thr	Leu	Asn	Pro	Lys	Ser
		690				695					700				
Glu	Asp	Pro	Asn	Thr	Leu	Arg</									

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770	775	780
Gly Lys Ile Ser Tyr	Lys Asp Leu Lys Asp	Gly Lys Tyr Gln Leu Ile
785	790	795 800
Glu Ala Val Ser Pro	Glu Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile	
	805	810 815
Leu Thr Phe Glu Val Val Lys Gly Ser Ile Lys Asn Ile Ile Ala Val		
	820	825 830
Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile		
	835	840 845
Thr Asn Thr His Ile Pro Pro Lys Gly Ile Ile Pro Met Thr Gly Gly		
	850	855 860
Lys Gly Ile Leu Ser		
865		
<210> SEQ ID NO 90		
<211> LENGTH: 5		
<212> TYPE: PRT		
<213> ORGANISM: Streptococcus agalactiae		
<400> SEQUENCE: 90		
Ile Pro Met Thr Gly		
1	5	
<210> SEQ ID NO 91		
<211> LENGTH: 858		
<212> TYPE: PRT		
<213> ORGANISM: Streptococcus agalactiae		
<400> SEQUENCE: 91		
Met Arg Lys Tyr Gln Lys Phe Ser Lys Ile Leu Thr Leu Ser Leu Phe		
1	5	10 15
Cys Leu Ser Gln Ile Pro Leu Asn Thr Asn Val Leu Gly Glu Ser Thr		
	20	25 30
Val Pro Glu Asn Gly Ala Lys Gly Lys Leu Val Val Lys Lys Thr Asp		
	35	40 45
Asp Gln Asn Lys Pro Leu Ser Lys Ala Thr Phe Val Leu Lys Thr Thr		
	50	55 60
Ala His Pro Glu Ser Lys Ile Glu Lys Val Thr Ala Glu Leu Thr Gly		
	65	70 75 80
Glu Ala Thr Phe Asp Asn Leu Ile Pro Gly Asp Tyr Thr Leu Ser Glu		
	85	90 95
Glu Thr Ala Pro Glu Gly Tyr Lys Lys Thr Asn Gln Thr Trp Gln Val		
	100	105 110
Lys Val Glu Ser Asn Gly Lys Thr Thr Ile Gln Asn Ser Gly Asp Lys		
	115	120 125
Asn Ser Thr Ile Gly Gln Asn Gln Glu Glu Leu Asp Lys Gln Tyr Pro		
	130	135 140
Pro Thr Gly Ile Tyr Glu Asp Thr Lys Glu Ser Tyr Lys Leu Glu His		
	145	150 155 160
Val Lys Gly Ser Val Pro Asn Gly Lys Ser Glu Ala Lys Ala Val Asn		
	165	170 175
Pro Tyr Ser Ser Glu Gly Glu His Ile Arg Glu Ile Pro Glu Gly Thr		
	180	185 190
Leu Ser Lys Arg Ile Ser Glu Val Gly Asp Leu Ala His Asn Lys Tyr		
	195	200 205
Lys Ile Glu Leu Thr Val Ser Gly Lys Thr Ile Val Lys Pro Val Asp		

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210	215	220
Lys Gln Lys Pro Leu Asp Val Val Phe Val Leu Asp Asn Ser Asn Ser 225 230 235 240		
Met Asn Asn Asp Gly Pro Asn Phe Gln Arg His Asn Lys Ala Lys Lys 245 250 255		
Ala Ala Glu Ala Leu Gly Thr Ala Val Lys Asp Ile Leu Gly Ala Asn 260 265 270		
Ser Asp Asn Arg Val Ala Leu Val Thr Tyr Gly Ser Asp Ile Phe Asp 275 280 285		
Gly Arg Ser Val Asp Val Val Lys Gly Phe Lys Glu Asp Asp Lys Tyr 290 295 300		
Tyr Gly Leu Gln Thr Lys Phe Thr Ile Gln Thr Glu Asn Tyr Ser His 305 310 315 320		
Lys Gln Leu Thr Asn Asn Ala Glu Glu Ile Ile Lys Arg Ile Pro Thr 325 330 335		
Glu Ala Pro Lys Ala Lys Trp Gly Ser Thr Thr Asn Gly Leu Thr Pro 340 345 350		
Glu Gln Gln Lys Glu Tyr Tyr Leu Ser Lys Val Gly Glu Thr Phe Thr 355 360 365		
Met Lys Ala Phe Met Glu Ala Asp Asp Ile Leu Ser Gln Val Asn Arg 370 375 380		
Asn Ser Gln Lys Ile Ile Val His Val Thr Asp Gly Val Pro Thr Arg 385 390 395 400		
Ser Tyr Ala Ile Asn Asn Phe Lys Leu Gly Ala Ser Tyr Glu Ser Gln 405 410 415		
Phe Glu Gln Met Lys Lys Asn Gly Tyr Leu Asn Lys Ser Asn Phe Leu 420 425 430		
Leu Thr Asp Lys Pro Glu Asp Ile Lys Gly Asn Gly Glu Ser Tyr Phe 435 440 445		
Leu Phe Pro Leu Asp Ser Tyr Gln Thr Gln Ile Ile Ser Gly Asn Leu 450 455 460		
Gln Lys Leu His Tyr Leu Asp Leu Asn Leu Asn Tyr Pro Lys Gly Thr 465 470 475 480		
Ile Tyr Arg Asn Gly Pro Val Lys Glu His Gly Thr Pro Thr Lys Leu 485 490 495		
Tyr Ile Asn Ser Leu Lys Gln Lys Asn Tyr Asp Ile Phe Asn Phe Gly 500 505 510		
Ile Asp Ile Ser Gly Phe Arg Gln Val Tyr Asn Glu Glu Tyr Lys Lys 515 520 525		
Asn Gln Asp Gly Thr Phe Gln Lys Leu Lys Glu Glu Ala Phe Lys Leu 530 535 540		
Ser Asp Gly Glu Ile Thr Glu Leu Met Arg Ser Phe Ser Ser Lys Pro 545 550 555 560		
Glu Tyr Tyr Thr Pro Ile Val Thr Ser Ala Asp Thr Ser Asn Asn Glu 565 570 575		
Ile Leu Ser Lys Ile Gln Gln Gln Phe Glu Thr Ile Leu Thr Lys Glu 580 585 590		
Asn Ser Ile Val Asn Gly Thr Ile Glu Asp Pro Met Gly Asp Lys Ile 595 600 605		
Asn Leu Gln Leu Gly Asn Gly Gln Thr Leu Gln Pro Ser Asp Tyr Thr 610 615 620		
Leu Gln Gly Asn Asp Gly Ser Val Met Lys Asp Gly Ile Ala Thr Gly 625 630 635 640		

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Gly Pro Asn Asn Asp Gly Gly Ile Leu Lys Gly Val Lys Leu Glu Tyr
 645 650 655
 Ile Gly Asn Lys Leu Tyr Val Arg Gly Leu Asn Leu Gly Glu Gly Gln
 660 665 670
 Lys Val Thr Leu Thr Tyr Asp Val Lys Leu Asp Asp Ser Phe Ile Ser
 675 680 685
 Asn Lys Phe Tyr Asp Thr Asn Gly Arg Thr Thr Leu Asn Pro Lys Ser
 690 695 700
 Glu Asp Pro Asn Thr Leu Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp
 705 710 715 720
 Val Arg Glu Tyr Pro Thr Ile Thr Ile Lys Asn Glu Lys Lys Leu Gly
 725 730 735
 Glu Ile Glu Phe Ile Lys Val Asp Lys Asp Asn Asn Lys Leu Leu Leu
 740 745 750
 Lys Gly Ala Thr Phe Glu Leu Gln Glu Phe Asn Glu Asp Tyr Lys Leu
 755 760 765
 Tyr Leu Pro Ile Lys Asn Asn Asn Ser Lys Val Val Thr Gly Glu Asn
 770 775 780
 Gly Lys Ile Ser Tyr Lys Asp Leu Lys Asp Gly Lys Tyr Gln Leu Ile
 785 790 795 800
 Glu Ala Val Ser Pro Glu Asp Tyr Gln Lys Ile Thr Asn Lys Pro Ile
 805 810 815
 Leu Thr Phe Glu Val Val Lys Gly Ser Ile Lys Asn Ile Ile Ala Val
 820 825 830
 Asn Lys Gln Ile Ser Glu Tyr His Glu Glu Gly Asp Lys His Leu Ile
 835 840 845
 Thr Asn Thr His Ile Pro Pro Lys Gly Ile
 850 855

<210> SEQ ID NO 92
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: amino acid linker

<400> SEQUENCE: 92

Gly Ser Gly Gly Gly Gly
 1 5

<210> SEQ ID NO 93
 <211> LENGTH: 5
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: cell wall anchor motif
 <221> NAME/KEY: VARIANT
 <222> LOCATION: (1)...(5)
 <223> OTHER INFORMATION: Xaa = Any Amino Acid

<400> SEQUENCE: 93

Leu Pro Xaa Thr Gly
 1 5

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What is claimed is:

1. A composition comprising:

(1) a Group B *Streptococcus* (GBS) antigen combination GBS, wherein the antigen combination consists of:

a first isolated Group B *Streptococcus* (GBS) polypeptide antigen, wherein the first isolated GBS polypeptide antigen is a GBS 80 polypeptide antigen comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, and SEQ ID NO:6, or an isolated fragment thereof comprising at least seven consecutive amino acids of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, or SEQ ID NO:6; and

a second isolated GBS polypeptide antigen, wherein the second isolated GBS polypeptide antigen is a GBS 322 polypeptide antigen comprising the amino acid sequence of SEQ ID NO:38 or an isolated fragment thereof comprising at least seven consecutive amino acids of SEQ ID NO:38; and

(2) adjuvant comprising a submicron oil-in-water emulsion of 5% squalene, 0.5% polyoxyethylene sorbitan monooleate, and 0.5% sorbitan trioleate.

2. The composition of claim 1, wherein the GBS 80 polypeptide antigen comprises the amino acid sequence of SEQ ID NO:3 or the fragment thereof comprising the least seven consecutive amino acids of SEQ ID NO:3.

3. The composition of claim 1, wherein the GBS polypeptide antigen is the isolated fragment, wherein the isolated fragment comprises the amino acid sequence of SEQ ID NO:7, SEQ ID NO:8, or SEQ ID NO:9.

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4. A composition comprising:

(1) a Group B *Streptococcus* (GBS) antigen combination, wherein the antigen combination consists of:

a first isolated GBS polypeptide antigen comprising the amino acid sequence of SEQ ID NO:7; and

a second isolated GBS polypeptide antigen comprising the amino acid sequence of SEQ ID NO:38; and

(2) an adjuvant comprising a submicron oil-in-water emulsion of 5% squalene, 0.5% polyoxyethylene sorbitan monooleate, and 0.5% sorbitan trioleate.

5. The composition of claim 4, wherein the first isolated GBS polypeptide antigen comprises the amino acid sequence of SEQ ID NO:3.

6. A method of producing the composition of claim 1 for raising an immune response against the GBS comprising combining the first isolated GBS polypeptide antigen, the second isolated polypeptide antigen, and the adjuvant to produce the composition.

7. A method of raising an immune response against *Streptococcus agalactiae* in a mammal, comprising administering to the mammal the composition of claim 1.

8. The method of claim 7, wherein the GBS 80 polypeptide antigen comprises the amino acid sequence of SEQ ID NO:3 or the fragment thereof comprising the at least seven consecutive amino acids of SEQ ID NO:3.

9. The method of claim 8, wherein the GBS 80 polypeptide antigen comprises the amino acid sequence of SEQ ID NO:3.

10. The method of claim 7, wherein the GBS 322 polypeptide antigen comprises the amino acid sequence of SEQ ID NO:38.

* * * * *